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Listing first 45 summaries
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                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length DB
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FEATURES source							COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 BG495857	
Location/Qualifiers 1562	Plate: LLCM1486 row: o column: 11 High quality sequence stop: 562.	found through the I.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	CDNA Library Preparation: CLONETECH Laboratories, Inc.	Tissue Procurement: ATCC	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 562)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	EST.	BG495857.1 GI:13457373	mRNA sequence. BG495857	н_мсс_59 но	BG495857 562 bp mRNA linear EST 27-MAR-2001		

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SOURCE
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
BG506209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 711)
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601860153F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4072428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 643.
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/lab_host="0H10B (Tl phage-resistant)"
/note="Organ: testis; Vector: PhR-LIB (Clontech); Site_1:
SfiI (9gccgctcggcc); Site_2: SfiI (9gccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
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/lab_host="NH10B (T1 phage-resistant)"
/note="Organ: lung: Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGACGACGACGACATG-dT2 (3)BN-3'
...tellong the company of the compa
                                                                                                                                                                                                                           /clone="IMAGE:4072428"
/clone_lib="NIH_MGC_61"
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/clone_lib="NIH_MGC_59"
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/db_xref="taxon:9606"
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Pred. No. 8.9e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iow
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iow
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM/21352 724 bp mRNA linear EST 01-UI-E-EO1-aib-b-20-0-UI.rl UI-E-EO1 Homo sapiens cDNA clone UI-E-EO1-aib-b-20-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mamumalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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/db_xrel="taxu:"Jour / db xrel="taxu:"Jour / db xrel="fettal" / dev_stage="fettal" / db xrel="fettal" / db xrel=
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a 145 c 165 g 177 t
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/db_xref="taxon:9606"
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Pred. No. 9.4e-20;
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REFERENCE
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BG034660
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TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
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602300022F1 NIH_MGC_87 Homo
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National Institutes of Health,
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM10089 row: 1 column: 05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                               Conservative
                                                                                                                                                         /organism="Homo.sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:4394260"
//clone=lib="NIH_MGC_87"
//tissue_type="mammary adenocarcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
//note="Organ: breast; vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC_Library."
155 c 178 g 214 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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Pred. No. 9.4e-20;
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                                                                                      AAATCCCACTTGAACCAACTGAAGAAAAGA
                                                                                                                                                                       TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 133
                                                                                                                                                                                                                                                              90;
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Tissue Procurement: ATCC
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National Institutes of Health, M
Unpublished (1999)
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                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccatcatgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCAGTGACGCGCGAATG-dT(3D)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                   Library."
184 c
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/db_xref="taxon:9606"
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/lab_host="DH10B (Tl phage-resistant)"
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Plate: LLAM13341 row: m column: 01
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                                                                                                                                                                                                                                                                             1088
AGENCOURT_6416157 NIH_MGC_71
5', mRNA sequence
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Tissue Procurement: ATCC/DCTD/DTP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1088)
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                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Cons
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/lab_host="0H10B (phage-resistant)"
/note="Organ: skin; Vector: pcMv-sporT6;
Site_2: Sall; Cloned unidirectionally. p
Average insert size 2 kb. Library const
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/db_xref="taxon:9606"
/clone="IMAGE:6065448"
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Chinese National Human Genon
351 Guo Shoujing Road, Zhang
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Insight into hepatocellular carcinogenesis at wanscriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad.
21625106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xu,x., Huang,J., xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
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/clone_Iib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="0H10B (phage-resistant)"
/note="Organ: uterus; Vector: pcMV-SPORT6
Site_2: Sall; Cloned unidirectionally. P
Average insert size 2.1 kb. "
8 a 218 c 255 g 294 t 3 others
                                                                                                                                                                                                            hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKC Homo sapiens cDNA clone GKCBYG04
                 /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                        /clone="GKCBYG04"
/clone_lib="GKC"
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/db_xref="taxon:9606"
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Road, Zhangjiang
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pBluescript sk(-); Site_1: EcoRI; Site_2:
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iang Hi-Tech Park,
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tionally. Primer:
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RESULT 9
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                               TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
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Fax: 410 614 0827
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41d3 Human retina cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dr. Jeremy Nathans, Dept. of Molecular Biology Johns Hopkins School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
Contact: Dr. Jeremy Nathans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: CTTTTGAGCAAGTTCAGCCTGGTTAAGT BACKWARD: GAGGTGGCTTATGAGTATTTCTTCCAGGGTAA Seg primer: GGGTAAAAAGCAAAAGAATT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: jeremy_nathans@qmail.bs.jhu.edu Clones from this library are NOT available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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cke, J., Smallwood, P. and Nathans, J.
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                                                                                        Conservative
                                                                                                                                                                  97
                                                                                                                                                            /lab_host="E. coli strain K802"
/note="Organ: eye; Vector: lambda gt10; Site_1: EcoRI; Site_2: EcoRI; The library used for sequencing was a sublibrary derived from a human retina cDNA library.

Inserts from retina cDNA library DNA were isolated, randomly primed, PCR amplified, Size-selected, and clor into lambda gt10. Individual plaques were arrayed and used as templates for PCR amplification, and these PCR products were used for sequencing."
                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone_lib="Human retina cDNA randomly primed sublibrary"
/sex="mixed (males and females)"
/tissue_type="retina"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 3.2e-19;
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primed sublibrary
                                                                                                      DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope
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1 (bases 1 to 987)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BE477083
BE477083.1 GI:9596688
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                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute.
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
Bovidae; Bovinae; Bos.
1 (bases 1 to 485)
Sonstegard, T.S., Ca
                                                                                        Bos taurus
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 280 c 180 g 284 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CS0DD008YN11"
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   Capuco, A.V.,
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Pred. No. 7.6e-18;
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sapiens cDNA clone CSODDO08YN11 3
 Van Tassell, C.P.,
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                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - Fr Web : www
                                                                                                                                          BP 191
Email:
                                                                                                                                                                                                            Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 922)
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Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bdlg. 200 Rm 2A, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Seq primer: ATTTAGGTGACACTATAG
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Fax: 301 504 8414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tads@anri.barc.usda.gov
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                                                                                                                                          segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="BARC 5BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled mRNA isolated from mammary tissues at eight physiological, developmental, and diserstates."

a 97 c 120 g 127 t
                  /clone_lib="LTI_NFL001_NBC4"
/sex="male"
                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="neuroblastoma cells"
                                                    /clone="CS0DD008YN11"
                                                                                                                        ocation/Qualifiers
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92.2%;
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1.9e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 631.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: Plate: LLCM944 row: 1 column: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4082070"
/clone="IMAGE:4082070"
/clone="IMAGE:4082070"
/clone="IMAGE:4082070"
/fissue_type="carrinoma, cell line"
/lab_host="DH10B (fl phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: place line RNA.
/not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ∕organism="Homo sapiens"
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97.8%;
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Pred. No. 6.6e-16;
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AAATCCCACTTGAACCAACTGAAGAAAAGA 90
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1 (Case 1 to 468)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
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Location/Qualifiers
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                                                                                                                                                                                          provided by Dr. Bertrand Jordan. Library went through rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                               (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two
                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
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                                                                                        AAATCTCACTTGCACCAATTGAAGAAAAGA
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                                                                                                                                                                                                                                                                 ; 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.MGI:1389158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 557)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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High quality sequence stop: 426.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Soares_mammary_gland_NMLMG"
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 A98668 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		4.4 4.5	C 42	41	39	3 <i>8</i>	c 36	C 334	· w ·	c 31	30	28 29	27	25 25	c 24	22 23	c 21	c 19	د	c 17	15	c 14	_ 	c 11	_		7	συ	441		ب ر	Result No. So
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                                                                  AGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACA
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	1980 1980	CTTTGAAATTTGCGAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTCTATTGAGT	وز وز	Qу Дъ	
	1920 1920	CTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGA	1861 1861	Qу	
,	1860 1860	TGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATT 	8 8	Фр	
	1800 1800	CTTTTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAA	1741 1741	Фр	
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	1680 1680	ACAGATTCCACATTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGGATTGACTGC	1621 1621	Оу	
	1620 1620	TAGTTCAGGAAAGCATTTTTTTTTTTTGAACCTTAAAGGTTCTATTAATAAAGCAGC	1561 1561	ф	
	1560 1560	TATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTGTGGGCTGATGTGTCTGGGAAATGATG 	1501 1501	ду Ду	
	1500 1500	TGCATAGCAGAAAAGCTCCCACCATTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCTC		ДУ	
	1440 1440	CAGGAGGGAGGGCTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTC	w w	дь	
	1380 1380	GAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTT [1321 1321	Qу	
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	1260 1260	GAAGAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTC	N N	dd	•
	1200 1200	CATCATTGGGGATCGCGAATGGGCACACATAAAATCCAAATCCCACTTGAACCAACT	1141 1141	dd Qy	
	1140 1140	GCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGTGATCGAAT	0 0	Qy Db	
	1080 1080	TCTTGAAATCG FGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGAT 	1021 1021	Qy Db	
	1020 1020	TGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAAGAGTCTGTTCTTGAACCTGC		Qy Db.	
	960	ATGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCC	901	Db	

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TITLE
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Matches 1258; Conserv
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GATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATT
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Regulation of physiological rates in Caenor tRNA-modifying enzyme in the mitochondria Genetics 159 (1), 147-157 (2001)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CILWLHADQAVLDERLDKRVDDMLAAGILEELEDFHRRYNOKINSENSQDYQHGIFQS
IGFKEFHEYLITEGKCTLETSNQLIKKGPGPIVPPVYGLEVSKWEESVLEPALEI
VQSFIQGHKPTATPIKMPYNEAENKRSYHLCDLCDRIIIGDREWAAHIKSKSHLNQLK
KRRRLDSDAVNTIESQSVSPDYNKEPKEKGSPGQNDQELKCSV"
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ivsadsmqvyegldiinkvsaqeqricrhhmisfvdplvtnytvvdfrnratalied
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/product="tRNA isopentenyl transferase"
/protein_id="AAL14107.1"
/db_xref="GI:16209579"
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/db_xref="taxon:9606"
/clone="c-2ec05"
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                                                                                            AGTTATCACCTGTGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCG 1168
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                                 GAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTT
                                                                                                       GTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCA 523
                                                                                                                                                                                 AAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAA
                                                                                                                                                                                                                                                       GCCCAAGAGAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTTGTGACC 283
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TTTGAAGAACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGT
                                                                     GAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTT 583
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/db_xref="taxon:9606"
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Golovko,A., Hjalm,G., Sitbon,F. and Nicander,B. Cloning of a human tRNA isopentenyl transferase Gene 258 (1-2), 85-93 (2000)
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Golovko, A. and Hjalm
Direct Submission
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SRPGPIVPPVYGLEVSDVSKWEESVLEPALEIVQSFIQGHKPTATPIKMPYNEAENKR
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                              BC010741
                                          Homo sapiens, Similar to tRNA isopen
clone MGC:17002 IMAGE:3905836, mRNA,
           MGC
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Direct Submission
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ORGANISM
Clone distribution: MGC clone distribution information through the I.M.A.G.E. Consortium/LLNL at: http://imag Series: IRAK Plate: 14 Row: p Column: 15 This clone was selected for full length sequencing bec passed the following selection criteria: matched mRNA Location/Qualifiers
                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site: http://www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-JUL-2001) National Institutes of Gene Collection (MGC), Cancer Genomics Office, Institute, 31 Center Drive, Room 11A03, Betheso
                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1844)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                          (Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
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                                                                                                                        information can be http://image.llnl.
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DMLAAGLLEELRDFHRRYNQKHVSENSOVDYHGHIFSNPCILMILHADQADERLDKRKD
DMLAKGLIELRDFHRRYNQKNVSENSOVDYHGHIFOSIGFKEFHEYLITEGKCTLETS
NOLLKKGIEALKOVTKRYARKONRWVKNRFLSRPGPIVPPVYGLEVSDVSKWEESVLE
PALEIYOSFIGCHKPTAFPIKMPYNEAENKRSYHLCDLCDRIIGDREWAAHIKSKSH
LNQLKKRRRLDSDAVNTIESQSVSPDHNKEPKEKGSPGONDQELKCSV"

374 C 454 9 471 t /protein_id="AAH10741.1" /db_xref="GI:14789611" transferase" 166. .1140 /lab_host-"DH10B" /clone="MGC:17002 IMAGE:3905836"
/tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71" /organism="Homo sapiens" /db_xref="taxon:9606" /product="Similar to tRNA isopentenylpyrophosphate /codon_start=1 /note="Vector: PCMV-SPORT6"

GACCTGGTCCCATTGTCCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGG 998 0; Pred. Score 765; Mismatches NO. 0 DB 9. 4. Length 1844; Indels Gaps

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REFERENCE
AUTHORS
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Homo sap
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Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL01383
                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                        Homo sapiens
           (sites)
                                                                                       1749 bp sapiens cDNA FLJ20061 fis,
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 Hikiji,T.,
 Kobatake, N.,
                Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                       mRNA linear clone COL01383.
Inagaki, H.,
                   Hominidae;
                             Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Scienc University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Similarity 99.6%;
21; Conservative
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LEPALEIVQSFIQGHKPTATPIKMPYNBAENKRSYHLCDLCDRIIGGREWAAHIKSK
SHLNQLKKRRRLDSDAVNTIESQSVSPDHNKEPKEKGSPGQNDQELKCSV"
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RESULT 7
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Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center: Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-546)
                                                                                          Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T. Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S. NEDO human cDNA sequencing project uppublished
                                                                                                                                                                            oligo capping; fis (full insert Homo sapiens colon cDNA to mRNA Homo sapiens
                                                            2 (bases 1 to 1749)
Sugano, S., Suzuki, Y., Ot
Shibahara, T., Tanaka, T.
                                                      Direct Submission
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AK074222.1 GI:18676765
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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T. and Nakamura,Y.
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, clone_lib:COL
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/clone="COLD1371"
/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                          AL Submitted (18-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CBH0 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 21, 1999 this sequence version replaced gi:6002299.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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                                                                                                VECTOR: pCYPAC2
This sequence is the entire insert of clone RP1-118J21 The true right end of clone RP1-117L23 is at 38518 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at
                                                                                                                                                                                                                                  The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-118J721 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human DNA sequence from clone RP1-118J21 on chromosome 1p34.1-35.3 Contains part of the gene for BMP8 (bone morphogenetic protein 8 (osteogenic protein 2)), an 1-myc-proto-oncogene, STSs, GSSs and CpG Islands.n, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                     http://www.sanger.ac.uk/HGP/Chrl.
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    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                 Location/Qualifiers
                                               .166496
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276'
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/note="
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                                                                 .14185
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repeat: matches 2129. .2417 of consensus"
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/work="match: proteins: Sw:P22004-Sw:P20722 Sw:P22003
Sw:P18075 Tr:Q9YCH7 Sw:P23359 Sw:P55105 Sw:P49003
Sw:P34820 Sw:P34821"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="dJ118J21.1 (bone morphogenetic protein 8 (osteogenic protein 2))"
/noteogenic protein 2))"
/noteo="match: cDNAs: Em:S77477 Em:X51801 Em:M97017 Em:U39545 Em:J04566 Em:X80992 Em:M60316 Em:M60315 Em:M97016 Em:X56906 Em:AF100787 Em:U40034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<830. .1098,3622. .3732,4242. .5153. .5347,14838. .14986,15379. .15568,28682. /gene="BMP8"
                                                                                                                                                                                         QREILAVLGLPGRPRPRAPPAASRLPASAPLFMLDLYHAMAGDDDEDGAPAERRLGRA
DLVMSFVNMVERDRALGHQEPHWKEFRFDLTQIPAGEAVTAAEFRIYKVPSIHLLNRT
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                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/product="dJ118J21.1 (bone morphogenetic protein
(osteogenic protein 2))"
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/db_xref="GI:7018292"
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complement(join(949. .1098,3622. .3732,4242. .4321,
5153. .5347,14838. .14986,15379. .15568,28682. .29015))
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/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                           translation="MTALPGPLWLLGLALCALGGGGPGLRPPPGCPQRRLGARERRDY/
52 repeat: matches 1691.
.1787
of consensus"
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2. .29381))
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YVETEDGHSVDPGLAGLLGQRAPRSQQPFVVTFFRASPSP1RTPRAVRPLRRRQPKKS NELPQANRLPG1FDDVHGSHGRQVCRRHELYVSFQDLGWLDWV1APQGYSAYYCEGEC SFPLDSCMNATNHAILQSLVHLMMPDAVPKACCAPTKLSATSVLYYDSSNNVILRKHF

/note="match: STS: Em:T63436" complement(4252. .4438) complement(4214. .4420) 2764. .2868 /note="FLAM_C repeat: matches repeat: matches 2002. ۲. .2438 of . 133 of consensus' consensus"

7787. 7873 /note="MIR repeat: matches 57. complement(8369. 8876) 'note≖"match: STS: Em:AA634039' MIR repeat: matches 19. luJb repeat: matches 1. . 146 .75 of consensus" .307 of consensus" of consensus"

/note="match: GSS: Em:B51067"

)427. .9746 /note="AluJb repeat: matches AluJb repeat: matches 1. . 312 . 296 of consensus"

'note="match: STS: Em: Z41229

evidence=not_experimental

/note-"L1MC3 repeat: 14186 ..14425 /note="L2 repeat: 13474. .13591 'note="AluJo/FRAM matches 957. repeat: matches matches 7071. .2141 of consensus" 178. .7691 of consensus" of consensus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 47. 16285. 16510
                                                                                                                                                                                                                                                           /note="67
30126 .30
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/note="AluSq repeat:
22705. .22759
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20785, ..20932
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20320. .20782
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15137. .15215
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23600. .23742
/note="MIR repeat: matches 8. .153 of consensus"
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                /note="L2 repeat: matches 2244 ..2278 of consensus" 32752 ..33074
                                                /note="22 copies 2 mer
32716 .32751
                                                                                  /note="L2 repeat: matches 32545 .32588
                                                                                                                                                     /note="MIR repeat: matches 81. .165 of 31389. .31662
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28542. .30030
/note="CpG island"
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26215. .26275
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23299. .23381
                                                                                                                    /note="AluSx repeat: matches 19.
31873...32143
                                                                                                                                                                                       /note="MIR repeat: matches 60. .241 of consensus"
30928. .31015
                                                                                                                                                                                                                           /note="L2 repeat: matches 2350. .2475 of consensus' 30283. .30460
                                                                                                                                                                                                                                                                                             /evidence=not_experimental
29451...29584
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28059. .28151
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/note="MIR repeat:
27580. .27733
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26604. .26643
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24618. .24684
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Chote="LTR16A repeat: matches 116. .325 of consensus"
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/note-"AluYb8
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repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 14, 2000 this sequence version replaced gi:7770499. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Bouslavkiy, L., Boukhgalter, B., Brown, A., Burkett, M., Collin Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
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1 (bases 1 to 200484)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-204L3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 204_L_3
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                   241 53099; contig of 1859 bp in length

100 53199; gap of 100 bp

54631; contig of 1432 bp in length

532 54731; gap of 100 bp

732 55751; contig of 1020 bp in length

752 55851; gap of 100 bp

152 57470; contig of 1619 bp in length

71 57570; gap of 100 bp

71 57570; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 20484: gap of 100 bp
85 21689: contig of 1205 bp in length
90 21789: gap of 100 bp
23191: contig of 1402 bp in length
92 23291: gap of 100 bp
92 24513: contig of 1222 bp in length
14 24613: gap of 100 bp
14 24613: gap of 100 bp
16 26235: gap of 100 bp
27 273: contig of 1388 bp in length
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45474: contig of 1321 bp in length
45574: gap of 100 bp
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16399: con
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46821: contig of 1247 t
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79: gap of 100 bp
40190: contig of 1711 bp in
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80: gap of 100 bp
44053: contig of 2173 bp
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19176: contig of 1272 bp in length
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17804: contig of 1305 bp in length
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123: contig of 1921 bp in
gap of 100 hr
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contig of 2173 bp in length
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contig of 1662 bp in length
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Matches
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                                                                                   1344
                                                                                                                                                                                                                                                                                                                               AAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACACT
AAGAGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACAT
                                                                                                                                                                                                                                                                                                                                                                                                              CAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACTATAACAAAGAACCTA
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97163: contig of 2493 bp in le
97164
97263: gap of
100 bp
97264
99724: contig of 2461 bp in le
99725
99824: gap of
100 bp
10352
103351: contig of 3327 bp in le
10352
103570: contig of 3119 bp in le
106471
10888: contig of 2418 bp in le
106471
10888: contig of 2418 bp in le
10889
10898: gap of
100 bp
10898: gap of
100 bp
11515
111614: gap of
111655
11360: contig of 2746 bp in le
114361: gap of
11461
11460: gap of
1100 bp
114361: contig of 3909 bp in le
118370
11839: gap of
11839: contig of 3900 bp in le
112360
12369: contig of 3900 bp in le
12360
12369: contig of 3900 bp in le
12360
12369: contig of 3910 bp in le
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77655 80277: conti
80278 80377: gap of
80378 81798: conti
81799 81898: gap of
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129407 13298
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86895 90311: contig of 3417 t
90312 90411: gap of 100 bp
90412 92255: contig of 1844 k
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100 bp in
100 bp
1137360: contig of 4276 bp in lengue
1137460: gap of
1137460: gap of
113746: contig of 3017
140476: contig of 3017
140576: gap of
129.1%:
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1 68623: contig of 2480
1 68723: gap of 100 bp
70122: contig of 1399
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80277: contig of 2623 bp in 1

80377: gap of 100 bp in 1

81798: contig of 1421 bp in 1

31898: gap of 100 bp in 1

34226: gap of 100 bp in 1
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                                                                                                                                                                                                                                                          199863 bp DNA 1i
Homo sapiens chromosome 1 clone RP11-473P22,
PROGRESS ***, 16 unordered pieces.
AL354888
Center project name: bA473P22
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 199863)
                  Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac:uk
----- Project Information
                                                                 Center: Sanger
                                                                                          requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version
                                                                                                                   Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgesh
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 189476 bases at least Q40 Consensus quality: 193311 bases at least Q30 Consensus quality: 195510 bases at least Q20 Insert size: 198363; sum-of-contigs Insert size: 201159; 6.2% error; agarose-fp Quality coverage: 3.87x in Q20 bases; sum-of-contigs Quality
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2378: gap of 100 bp
22743: contig of 20365 bp in length
22843: gap of 100 bp
45183: contig of 22340 bp in length
45283: gap of 100 bp
45283: gap of 100 bp
45283: gap of 4298 bp in length
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14646: contig of 36510 bp
145892: cont':
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93481: contig of 6829 bp
93581: gap of 100 bp
101614: contig of 8033 bp
101714: gap of 100 bp
101716: config of 6122 bp
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199863: contig of
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58258: contig of 8577 k
58: gap of 100 bp
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Patent: W
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 6.8e-120;
0; Mismatches 2;
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Eukaryota; Metazoa; G
Mammalia; Eutheria; I
1 (bases 1 to 252)
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Primer B: AG
STS size: 20
PCR Profile:
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                                                                                                                                                                                                                                                                                                             Buffer:
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Fax: 617 252 1902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
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Primer: each 5 pM
dNTPs: each 4 nM
Tag Polymerase: 0
Total Vol: 20 ul
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nilarity 99.2%;
Conservative
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                                                                                                                                                                                                                                                                                MgCl2: 1.5 mM
KCl: 50 mM
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                                                                                                                                                                                                                                                                                                                                                                                                                   Thermal Cycler:
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                                                                                                                                 /map="122.8 cR from top 48. 248 48. 72
                                                                                                      complement(225. 58 c 34
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                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAATTTACAAG 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 189476 bases at least Q40
Consensus quality: 193311 bases at least Q30
Consensus quality: 195510 bases at least Q20
Consensus quality: 195510 bases at least Q20
Insert size: 198363; sum-of-contigs
Insert size: 201159; 6.2% error; agarose-fp
Quality coverage: 3.87x in Q20 bases; sum-of-contigs Quality
Coverage: 3.98x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced gi:9213379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: bA473P22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Sanger Centre
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AL354888.6 GI:9863692
AL354888.6 HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 199863)
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HOMO Sapiens chromosome l clone RP11-473P22, *** SEQUENCING PROGRESS ***, 16 unordered pieces.
                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is rarbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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1 2278: contig of 2278 bp in length
279 2378: gap of 100 bp
379 22743: contig of 20365 bp in length
744 22843: gap of 100 bp
844 45183: contig of 22340 bp in length
847 45283: gap of 100 bp
848 45283: gap of 100 bp
849581: contig of 4298 bp in length
849581: gap of 100 bp
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64183
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86653. .
                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:01156
fragment_chain:3"
93582...101614
/note="assembly_fragment:00528'
167976. .183411
                                                      /note="assembly_fragment:00307"
155993. 167875
                                                                                                                                       /note="assembly_fragment:01896
fragment_chain:4"
                                                                                                                                                                                                                            /note="assembly_fragment:00867
fragment_chain:4"
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fragment_chain:3"
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fragment_chain:1"
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                                                                                                                  144647.
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_fragment:00339
fragment_chain:3"
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fragment_chain:2"
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72764: contig of 8582 bp in length
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64082: contig of 5724 bp in length
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                                                                                                                                                                                                                                                                                                                          Grand-Pierre, N. Grant, G. Hagos, B. Heaford, A. Horton, L. Howland, J. C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Murphy, T., Naylor, J., Peterson, K., Pierre, N., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Voung, G., Zainou, J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 79785)
Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 1, clone RP11-21702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome 1 clone RP11-21702 map 1, SAMPLING.
                                                                                                                          on Mar 26, 2000 this sequence version replaced given All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D. Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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                                                                                                                                                                                                                       Submitted (04-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 26, 2000 this sequence version replaced gi:7158126.
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                                                    Center: Whitehead
Center code: WIBR
Contact: sequence_submissions@genome.wi.mit.edu
                             Web site: http://www-seq.wi.mit.edu
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LOW-PASS SEQUENCE
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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11326: contig of 733 bp in
11327 11426: gap of 100 bp
11427 12137: contig of 711 bp in
12138: 12237: gap of
                                                                                                                                                                                                                                 17006 17105: gap of 100 bp
17106 17925: contig of 720 bp
17826 17925: gap of 100 bp
17926 18639: contig of 714 bp
18640 18739: gap of 100 bp
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592 9791: gap of 100 bp
792 10493: contig of 702 bp in 16
94 10593: gap of 100 hp
94 117376.
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4 16283: gan
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22: contig of 7
2238: cc
8:
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                                                                               20269: contig of 712 bp i
369: gap of 100 bp
1069: contig of 700 bp
169: gap of 100 bp
21895: contig of 726 bp i
                                                                                                                                                               20269: cont
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j: gap of
22709:
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15372: contig of 720 bp
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23507: contig
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34932 35627: contig of 696 bp in length
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28 36446: contig of 719 bp
47 36546: gap of 100 bp
47 37245: contig of 699 bp
47 37345: gap of 100 bp
48 37345: gap of 32 bp
78 38177: gap of 702 bp
78 38177: gap of 100 bp
80 38979: gap of 100 bp
80 39688: contig of 702 bp
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50 26849: gap of 100 bp

50 27562: contig of 713 bp in 16

3 27662: gap of 100 bp

53 27662: gap of 100 bp

53 28369: contig of 707 bp in 1e

60 28469: ann of 707 bp in 1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29971; contig of 718 bp
72 30071; gap of 100 bp
2 30770; contig of 699 bp
1 30870; gap of 100
31501
                                                                      51923:
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42116: contig of 699 bp
42216: gap of 100 bp
42923: contig of 707 bp
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24397: gap of
25107: contig of
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                                   9514: gap of 100 bp 50220: contig of 706 bp 1 00320: gap of 100 bp 51010: contig of 690 bp 1 1110: gap of 100 bp 51823: contig of 713 bp 1 52648: contig of 725 bp 1 72748: days of 725 bp 1 00 bp 51823: contig of 725 bp 1
                                                                                                                                                                                                                    47789: contig of 703 bp i
7889: gap of 100 bp
48590: contig of 701 bp i
8690: gap of 100 bp
49414: contig of 724 bp i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3788: gap of 1712 bp 40500: contig of 712 bp 100 bp 100 pr 1717 bp
                                 52648:
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34012: contig of 1
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    748: gap of 53466: con
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26749:
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43739: contig of
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31581: contig of 711 br
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FEATURES

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 41 Row: 1 Column: 20.

source

CDS

/codon_start=1 /product="RIKEN CDNA 2310075G14 /protein_id="AAH19812.1" /db_xref="GI:18044186"

gene"

/clone="MGC:30541 IMAGE:5042856" /tlssue_type="Kidney, normal. 5 /clone_lib="MCI_CGAP_Kid14" /lab_host="DH10B"

month

old

male mouse.

/map="EVB/N"

/organism="Mus musculus" /db_xref="taxon:10090"

Location/Qualifiers l. .2045

/note="Vector: pCMV-SPORT6"

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COMMENT
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ORGANISM
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120; Conservative
Gunaratne, P.H., Garcia, A.M., Lu, Yoon, V.S., Kowis, C.R., Lawrence, Richards, S., Gibbs, R.A.
                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                      Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: amg@bcm.tmc.edu
                                                                                                                  Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGC
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IMAGE:5042856,
                                                                                                Center code: BCM-HGSC
                                                                                                                                DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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57 54295: contig of 729 bp in 14

96 54395: gap of 100 bp in 14

96 55105: contig of 710 bp in 14

96 55205: gap of 100 bp

96 55935: contig of 730 bp in 14
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RIKEN cDNA 2310075G14 gene, clone MGC:30541
, mRNA, complete cds.
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                  X., Hulyk, S.W., Hale, S.M. S., Martin, R.G., Muzny, D.
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BASE COUNT ORIGIN Query Match 2.4%; Score 48; DB 10; Length 2045; Best Local Similarity 100.0%; Pred. No. 3.3e-14; Matches 48; Conservative 0; Mismatches 0; Indels 570 a

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Gaps

0;

Search completed: April 21, 2003, 21:27:10 Job time: 6769 secs

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BM800217 AGENCOURT BG612651 602640078 AV759288 AV759288

AI718450

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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 573
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10050.164 Million cell updates/sec
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REFERENCE

TITLE AUTHORS

FEATURES

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ACCESSION VERSION

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                                                                                             BM975520 743 bp mRNA UI-CF-EN1-acw-c-07-0-UI.sl UI-CF-EN1 Homo UI-CF-EN1-acw-c-07-0-UI 3', mRNA sequence
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 743)
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/dev_stage="fetal"
/lab_host="MC1061/P3"
/note="Vector: pCDNA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of CDNA Library preparation: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA sequence: 1-56, >AT_rich#Low_complexity (matched compliment)
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                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="Adult"
//dev_stage="Adult"
//dev_stage="PH108 (Life Technologies) (T1 phage resistant)"
//note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: Ecor I; Site_2: Not I; U1-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.
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TAG_SEQ=CTGCTCAGGT"
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TAG_TISSUE-Human Lung Epithelial Cell Lines untreated LPS
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/clone_lib="UI-CF-EN1"
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                                                                                                                                                   Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
                                                                                                                                                                                                            21C Frontier Korean EST Project 2001 Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                     mRNA sequence
BM847727
                                                                                                                                                                                                                                                                                                                                                                           BM847727 578 bp
K-EST0127301 S13KMS5 Homo sapiens
                                                                                                        Email: yongsung@mail.kribb.re.kr
plate: 50 row: D column: 09
High quality sequence stop: 578.
                                                                                                                                           Fax: +82-42-860-4409
                                                                                                                                                                                                    Contact: Kim YS
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                                                                                                                                                                                                                                                                                                                                          BM847727.1 GI:19204126
                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F'"
                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                              J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
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150
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               D
strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

143 c 160 g 125 t
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DB 14;

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578
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                                                                                                                                                                                                                  Match 26.5%;
Local Similarity 100.0%;
                      GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCT
                                                                                             CGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGG
                                                                                                                    AATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCC
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BE315223.1 EST.

mRNA sequence BE315223

BE315223 601141778F1 NIH_MGC_9

Homo

sapiens

cDNA clone

IMAGE: 3141643

EST 26-OCT-2000

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                            GGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGAT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 725)
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plate: LLCM111 row: k column: 20
High quality sequence stop: 720.
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: Ovary; Vector: pOTB7; Site_1: XhOI; Site_2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected > 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 175 c 197 g 167 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
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/clone="IMAGE:3141643"
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Pred. No. 5.6e-186;
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Contact: Chenggang Zhang
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1 (bases 1 to 601)
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27 Taiping Road, I
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Taiping Road, Beijing 100850, P.R.China
ail: zhang_chenggang@hotmail.com.
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/db_xref="taxon:9606"
/clone_lib="Human fetal liver
/tissue_type="liver"
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Pred. No. 9.5e-168;
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603023811F1 NIH_MGC_114
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                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
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National Institutes of Health, Mammalian
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Location/Qualifiers
                                  207
                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194347"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
                               /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019: Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1088)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12212 row: j column: 17
High quality sequence stop: 651.
Location/Qualifiers
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Tissue Procurement: ATCC
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/Ob_xref="taxon:9606"
/Ob_xref="taxon:9606"
/Clone="IMAGE:5531248"
/Clone=Ltype="leiomyosarcoma"
/Lissue_type="leiomyosarcoma"
/Lab_host="DH10B (phage-resistant)"
/Lab_host="DH10B (phage-resistant)"
/Note="Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not. Site_2: Sall; Cloned unidirectionally. Primer: Oligo (Average insert size 2.1 kb. ."
Average insert size 2.1 kb. ."
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BG612651
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GAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACATGTCC 1347
                                                                                                                                                         AAGTTATCACCTGTGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGC
                                                                                                  TGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCAGACTATAACAAAGAACCTAAAAGG
                                                                                TGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACCATAACAAAGAACCTAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
1 (bases 1 to 869)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 684.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="embryonal carcinoma"
/lab host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCGAGGCGGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
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/clone_lib="NIH_MGC_61"
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/db_xref="taxon:9606"
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CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H. Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Ze,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Homo sapiens cDNA MDS clones
Oppublished (2000)
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AV759288 MDS Homo sapier
AV759288
AV759288.1 GI:10917136
                                                                                                                                                                                                                                                                                                                                                                                                                         201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
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                                                                                                                                                                                                                                                           166
                                                                                                                                                                                  Conservative
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lone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MDS Homo sapiens
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                    /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                 /clone="MDSBLH01"
/clone_lib="MDS"
                                                                                                                                                                                                                                                        /note="vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB"
158 c  175 g  139 t  1 others
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                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI718450.1
                                                                                                                                                                                                                                                                                                                                IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
                                                                                                                                                                                                                                                                                                High quality sequence stop: 447.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 559)
                 191
                                                           the modified pT7T3 vector. Library constructed by Bob Barstead."

118 c 84 g 166 t
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2332692"
                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                        /lab_host="DH10B (phage resistant)"
                                                                                                                                                                                                                       /clone_lib="Barstead colon HPLRB7"
                                                                                                                                                                                          /dev_stage="adult, age 25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA linear
Homo sapiens cDN
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Query Match Best Local :

Similarity

19.0%; 99.6%;

Score Pred.

388; DB 9; No. 1.2e-133;

Length 559;

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REFERENCE
AUTHORS
TITLE
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SOURCE
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                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                        624 bp mRNA linear EST 26-MAR UI-H-EII-ayx-n-12-0-UI.sl NCI_CGAP_EI1 Homo sapiens cDNA clone mAGE:5845067 3', mRNA sequence.
                                         CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.linl.gov The following repetitive elements were found in this cDNA sequence: 1-36, >POLY_A#Simple_repeat (matched compliment)
                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
                 Seq primer: M13 FORWARD POLYA=Yes.
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                          Homo sapiens
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                AAAATTATCTAATTTCCAGATGCTTTTGTAGATGACTGAAGTATTTGTGAGCCACATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="DH10B (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I
NCI_CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_SEQ=ACACTTGCAC*
128 c 97 g
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                                                            TTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCT
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                                                                                                                                                                                      CTGATTGAAGATATATTTGCCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTAT
ACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAA
                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11252 row: d column: 20
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602941574F1 NIH_MGC_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: cervix: Vector: pCMV-SPORT6; Site_1: Not Site_2: SalI; Cloned unidirectionally. Primer: Oligo Average insert size 1.4 kb. Library prepared by Life Technologies."

181 c 184 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5104483"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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E:5104483 5',
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1 GGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACATGTC

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1287 GGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACATGTC 1346
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                                                     435;
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1 (bases 1 to 457)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J. Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashUn-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA121465 457 bp mRNA zk91c07.r1 Soares_pregnant_uterus_NbHPU IMAGE:490188 5', mRNA sequence.
AA121465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 419.
Location/Qualifiers
                                                                                                                                        119
                                                    Conservative
                                                                                                                                   /note=""Updan: uterus; vector: pT/T3-Pac; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5']
AACTGGAAGAATTCGGGCCGCTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."

a 82 c 112 g 142 t 2 others
                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                             /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                 /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:3804775"
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                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_pregnant_uterus_NbHPU"
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                                                                    18.9%;
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                                                                    Score 385; DB 9;
Pred. No. 1.9e-132;
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                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qe70f07.x1 Soares_fetal_lung.NbHL19W Homo sapiens cDNA clone IMAGE:1744357 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
181
                                                                                                                                                                                                                                                         quality sequence stop: 472.
Location/Qualifiers
      /clone_lib="Soares_fetal_lung_NbHL19W"
/dev_stage="19 weeks"
                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                 /lab_host="DH10B (ampicillin resistant)"
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 562)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) upublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC
        cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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                                                                                      AGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTCCCAC 1462
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Location/Qualifiers
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/tisue_type="mucoepidermoid carcinoma"
/lab_host="DHHOB (T1 phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_2: SfiI (ggccattatggcc);
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CAGGCCGATTATGGC-3' and 3' adaptor
sequence: 5'-CAGGCCGACGTTATGGC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGGCGCCACATG-dT(30)BN-3'
(where B - A, C, or G and N - A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Library."
122 c
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/db_xref="taxon:9606"
/clone="IMAGE:4671586"
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Command line parameters:

MODEL-frame+_n2p.model -DEV-xlh
-Q-/Ggn2_J/USPTO_Spool/US09513151/runat_15042003_141144_26380/app_guery.fasta_1.2446
-Q-/Ggn2_J/USPTO_Spool/US09513151/runat_15042003_141144_26380/app_guery.fasta_1.2446
-DB-SPTREMBL_21 -QFMT-fastan -SUFFIX-n2p.rspt -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40 cdi
-LIST-45 -DOCALLGN-200 -THT_SCORE-pct -THR_MAX-100 -THR_NIN-0 -ALIGN-15
-MODE-LOCAL -QUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09513151_@CGN_1_1_125 @runat_15042003_141144_26380 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPEXT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                    GTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAACGCCTA
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MEDLINE=20564178; PubMed=11111046;

X MEDLINE=20564178; PubMed=11111046;

A GOLOVKO A., Hjalm G., Sitbon F., Nicander B.;

AT "Cloning of a human tRNA isopentenyl transferase.";

RL Gene 258:85-93(2000).

DR EMBL; AF074918; AA631324.1; -.

DR InterPro; IPR002627; IPPT.

DR InterPro; IPR002627; IPPT.

DR InterPro; IPR000822; Znf_C2H2.

DR Pfam; PF01715; IPPT; 1.

DR ProDom; PD004674; IPPT; 1.

DR TIGREAMS; TIGR00174; miaA; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
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09-513-151-3
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
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                   3.91e-180
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GluProAlaLeuGluIleValGlnSerPheIleGlnGlyHisLysProThrAlaThrPro
               GAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCA
                            CAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTG
                                                                                                                                                     ArgArgTyrAsnGlnLysAsnValSerGluAsnSerGlnAspTyrGlnHisGlyIlePhe
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A Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shil
A Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AKOOO068; BAA90923.1; -.
R InterPro; IPR0002627; IPPT.
R InterPro; IPR0002627; IPPT; 1.
R Pfam; PF01715; IPPT; 1.
R Pfam; PF01715; IPT; 1.
R Pfonom; PD004674; IPPT; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
CDNA FLJ20061 fis, clone COL01383.
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Mammalia; Eutheria; F
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Q96FJ3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to tRNA isopentenylpyrophosphate transferase.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Butheria; Primates; Catarrhini; Hominidae;
Submitted (JUL-2001) to the EMBL; BC010741; AAH10741.1; InterPro; IPR002627; IPPT. InterPro; IPR000822; Znf_C2H
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Znf_C2H2
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Best Local Similarity:
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probom; PD004674; IPPT; 1.
SMART; SM00355; ZDF_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_
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                                                                      AAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGTGAT
         CGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAAC
                                                                                                                                    CCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAA
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Mismatches:
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ EMBL; AK003556; BAB22853.1; -. EMBL; BC019812; AAH19812.1; -. MGD; MGI:1914216; 2310075614Rik. InterPro; IPR002677; IPPT. InterPro; IPR000822; Znf_C2H2. Pfam; PF01715; IPPT; 1. Proc. Proc. (19000822); Znf_C2H2.
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SEQUENCE FROM N.A.
TISSUE-EMBRYO
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                                                                                                                                                                                                                                                                                      Prodom; PD004674; IPPT; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

SEQUENCE 326 AA; 37191 MW; 454367A8B70DD1F0
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Saito R.,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 49.5 kDa protein (TRNA isopentenyl transferase).
2C395.6 OR GRO-1.
                                                                                                                                                                                                                                                                     Local Similarity:
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002627; IPPT.
InterPro; IPR00822; Znf_C2H2.
Pfam; PF01715; IPPT, 1
PF080715; IPPT, 1
PR0517E; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
Hypothetical protein; DNA-binding; Transferase; Zinc-finger.
SEQUENCE 430 AA; 49548 MW; 107E95095C81A2B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                               "Regulation of Physiological Rates in Caenorhabditis trNA-Modifying Enzyme in the Mitochondria."; Genetics 159:147-157(2001).
EMBL; U13642; AAGG0042.2; -.
EMBL; AY052773; AAL14112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lemieux J., Lakowski B., Webb
Barnes T., Hekimi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Direct Submission.";
Submitted (DEC-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans Submitted (NOV-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connell M.;
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SpAC343.15.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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                                                                                                               GAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTT 583
                            TyrPheHisThrGlyArgProProSerGluIleTyrSerGluGlnLysMetLysSerSer 194
                                                                                                                                                                            GTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCA 523
                                                                                                                                                                                                                                                                                                                        ArgValIleAspGluIleHisSerGlnGlyLysIleProIleValValGlyGlyThrHis 102
                                                                                                                                                                                                                                                                                                                                                                                                                                           AspThrIleThrAsnLysIleThrValGluGluGluGluAsnValHisHisArgLeuMet 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGAAGAAACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGT
                                                                                   ValMetAlaGluGlnTrpHisProArgAspThrArgLys!leArgArgSerLeuGluIle
                                                                                                                                                                                                                                    AAT-----ACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAA 463
                                                                                                                                                                                                                                                                 TyrTyrLeuGlnSerLeuLeuPheGluAspThrThrLeuSerAlaIleAspLysLeuThr 122
                                                                                                                                                                                                                                                                                             GCTCTGATTGAAGATATTTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAAT 379
                                                                                                                                                                                                                                                                                                                                                                                  SerPheLeuAsn---PheAspLysGluTyrSerValProGluPheGluArgAspAlaSer
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                                                                                                                                               -----AspAspProSerAlaMetLeuSerTyrLeuLysLysIleAspPro 154
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Q9ZUX7 PRELIMINARY; PRT; 466 AA. Q9ZUX7; Q9SQ59; Q9TY7; Q9SQ59; Q1-JUN-2002 (TrEMBLrel. 10, Created) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Las	1154 CGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGAAGA 1213 :::::::::::::::::::::::::::::::::::	15CACCTGTGTGACCTCTGTGATCGAATCATCATTGGGGAT 115CACCTGTGTGACCTCTGTGATCGA	1091 GAAGCTGAGAACAAGAGAAGTTAT	1031 GTGCAAAGTTTCATCCAGGGCCACAAGAGCCTACAGCCACTCCAATAAAGATGCCATACAAT 1090	971 TTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATC 1030 ::: :::::	938PheSerThr 320 938PheSerThr 320	914	875 CACGAGTACCTG913 :::	824AGCCAGGACTATCAACATGGTATCTTCCAATCAATTGGCTTCAAGGAATTT 874 ::: :::	764 CTCTTGGAGGAACTAAGAGATTTTCACAGAGGCTATAATCAGAAGAATGTTTCGGAAAAT 823 :::::: :::: :::::: :::: ::::::: ::::: ::::::: ::::::	704 GACCAGGCAGTTCTAGATGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCT	

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Percent Similarity:
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Pred. No.:
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EMBL; AC005824; AAC73024.2; -.
EMBL; AF109376; AAF00582.1; -.
EMBL; AB063609; BAB59042.1; -.
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InterPro: IPR000822; Znf_C2H2.
InterPro: IPR000690; Znf_matrin.
Pfam; PF01715; IPPT; 1.
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GOLOVKO A., Hjalm G.;
"A tRNA isopentenyl transferase from Arabidopsis thaliana."
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Town C.D., Kaul S.;
Submitted (FEB-2002)
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ProDom; PD004674; IPF; 1.
SMART; SM00355; ZnF_C2H2; 1.
TIGRFAMS; TIGR00174; miaA; 1.
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SEQUENCE FROM N.A.
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  GATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTG
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                                                   AlaAspValAlaSerValValAspGlnAspMetValValGluSerValPheGlyArgAsp 162
                                                                                                                                                                                                           CTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCCAGGAGATGGGCACTGAGAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGAT 334
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Adenylate Isopentenyltransferase,
Arabidopsis thaliana.";
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Q1-JUN-2002 (TrEMBLrel.
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                                                                                                       Asn
                                                                                                                                                              ThrThrArgHisLysAsnSerGlnThrTyrLysAsnArgGluValGlnGluAlaGluVal
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:OJ1656_A11_";
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Eukaryota; Viriddiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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tRNA delta(2)-isopentenylpyrophosphate transferase.
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MEDLINE=21992816; PubMed=11997336;
            SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                        Thermoanaerobacteriales;
                                                                                   Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
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EMBL; AE013095; AAA24581.1; -.

Transferase; Complete proteome.

SEQUENCE 315 AA: 36841 MW; 61DCA4A2D5EC
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IleGlnIleValLeuIleValGlyProThrAlaThrGlyLysSerArgLeuAlaValAsp
 ATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGC
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                                           LeuLysIleGlyTyrAsnLysTyrGlyThrSer--
                                                                       CACAGA----CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCCAGGACTATCAACATGGT
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Yu J., Yang H.;
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submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AP003455; BAB85364.1; -
SEQUENCE 427 AA; 44773 MW; 316568B1DC5F62F
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-JUN-2002 (TrEMBLrel.
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 GATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTG
                                                                          ValAlaGlyGlySerAsnSerLeuIleHisAlaLeuLeu-----
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                                                                                                                            PheArgSerLeuAlaAlaAlaAlaAlaGlyIleAlaSerArgGlyArgValProVal
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RESULT 12
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SEQUENCE FROM N.A.
Bevan M., Wedler H., Wedler E., Wambutt R., no
Mayer K.F.X., Schueller C.;
Mayer K.F.X. (FEB-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative tRNA isopentenyltransferase (Adenylate
isopentenyltransferase) (Cytokinin synthase) (EC 2.5.1.27).
F22K18.150 OR ATG24650 OR ATIPT4.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid.
Encasids II; Brassicales; Brassicaceae; Arabidopsis.
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                          SEQUENCE FROM N.A. Wedler E. Submitted (MAR-2000)
                                                                                     EU Arabidopsis sequencing project; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ
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SEQUENCE FROM N.A
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                            Wambutt R., Mewes H.W., to the EMBL/GenBank/DDBJ
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EMBL; ALI61561; CAAP3375 1; -
EMBL; AB662611; BAB59044.1; -
EMBL; AB661402; BAB590311; -
InterPro; IPRO2627; IPPT; 1.
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Takei K., Sakakibara H., Sugiye
"Identification of Genes Encod:
Cytokinin Biosynthesis Enzyme,
J. Biol. Chem. 0:0-0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WASSILEWSKIJA;
Matsumoto M., Kakimoto T.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
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Encoding Adenylate Isopentenyltransferase,
nzyme, in Arabidopsis thaliana.";
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Conservative:
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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"Arabidopsis cytokinin synthase.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL, AB661405; BAB59033.1; -.
InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
ProDom; PD004674; IPPT; 1.
SEQUENCE 329 AA; 36965 MW; C78C692FE957CCC
                                                                                                                                                                                                                                                         STRAIN=WASSILEWSKIJA;
Matsumoto M., Kakimoto T.;
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse:ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-WASSILEWSKIJA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGATTGAAGATATTTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                valLeuThrAsnLysValThrProLysGluCysArgGlyValProHisHisLeuLeuGly
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                                                                                                            CAGCTTCTA----
                                                                                                                                                 ValProGluLeuHisGluTyrLeuArgAsnGluSerLeuValAspArgAlaThrLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTTCTCCAT
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                                                                                                                                                                                             TTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAGACTAGTAAC
                                                                                                                                                                                                                                                                                                                                                                                                          CysPheIleTrpValAspValSerLeuProValLeuAsnSerPheValSerLysArgVal
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                                                                                                            ----AAGAAAGGACCTGGTCCCATTGTC-----
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Matches:
Conservative:
Mismatches:
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                        -CCCCCTGTCTATGGCTTAGAG
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191 802 174 742 154

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976 245 955 225 922 622

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140

135

382

Qy 83 CTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGC 142	DR EMBL; AB062613; BAB59046.1; DR InterPro; IPR002627; IPPT. DR Pfam; PF01715; IPPT; 1. DR ProDom; PP004674; IPPT; 1. KW Transferase. SQ SEQUENCE 329 AA; 36979 MW; 66AFA61D3DE49AF8 CRC64; Alignment Scores: Pred. No.: 333.50 Matches: Percent Similarity: 38.94% Dest Local Similarity: 9.33% Query Match: 10 US-09-513-151-3 (1-2041) x Q9LUG4 (1-329) US-09-513-151-3 (1-2041) x Q9LUG4 (1-329)		RESULT 14 Q9LUG4 Q9LUG4 ID Q9LUG4; AC Q9LUG4; DT 01-CCT-2000 (TrEMBLrel. 15, Created) DT 01-CCT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-DUN-2002 (TrMBLrel. 15, Last annotation update) DT transferase) (Last annotation update) DE tran isopentenyl transferase-like protein (Adenylate DE isopentenyltransferase) (EC 2.5.1.27). GN ATIPT). OS Arabidopsis thaliana (Mouse-ear cress). OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; OX NCBL_TaxID-3702; RN [1] RP SEQUENCE FROM N.A. RC STRAIN-COLUMBIA; RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; RA Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.	Db 246 GlnLeuLysLysIleGlnArgLeuHisLysLysTrpLysMetSerMetHisArgValAsp 265 Oy 977 GTATCTGATGTGTCGAAGTGGAAGGAGTCT 1006 !!!!!!! Db 266 AlaThrGluValPheLeuLysArgAsnValGluGlnAspGluAlaTrpGluAsnLeu 285 Qy 1007 GTTCTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCC 1066 !!! Db 286 ValAlaArgProSerGluArgIleValAspLysPheTyrAsnAsnAsn
OY 1067 ACTCCAATAAAGATGCCATACAATGAAGCTGAGAACAAGAAGTTATCACCTGTGTGAC 1126	CAGCTTCTAAGAAAGGACCTGGTCCCATTGTC	Oy 683 TGCATCCTTTGGCTTCATGCCGACCAGGCAGTTCTAGATGAGCGCTTGGATAAGAGGGTG 742		

DDR RRAC S S S S S P P F E E S S K S S S S P P F E E S S K S S S P P P F E E S S K S S S P P P F E E S S K S S S P P P F E E S S K S S S P P P F E E S S K S S S S P P P F E E S S K S S S S P P P F E E S S K S S S S S S P P P F E E S S K S S S S S S S P P P F E E S S K S S S S S S S S S S S S S S S	11127 313 313 313 313 313 313 313 313 313 31	1127 CTCTGTGATCGAATCATCATCAGGATCGCGAATGGGCACGCAC
	Arabi Arabi Eukai Eukai Sperm Sperm euros	iana (Mouse-ear cress). iplantae: Streptophyta; Embryophyta; Tracheophyta; agnoliophyta; eudicotyledons; core eudicots; Rosida ssicales; Brassicaceae; Arabidopsis.
	SEQUI SEQUI STRAI Matsu	A. KIJA; Kimoto T.; 001) to the EMBL/GenBank/DDBJ database
	[2] SEQUI	A. KIJA:
	Kakin "Arak	okinin synthase.";
	EMBL;	TO THE EMBL/GenBank/DDBJ database 9032.1; IPPT.
	Prode	m; PD004674; IPPT; 1. NCE 330 AA; 37408 MW; 0F440B0A4237CD02 CRC64;
Alignme Pred. N Score: Percent Best Lo Query M DB:		es: rity: ilarit
0S-09	-513-	151-3 (1-2041) x Q94ID2 (1-330)
Db Qy	20	GTGGCGGCTGCACGAGCAGTTCCTGTGGGGCAGTGGGCTCAGGGGGCCTGCAACGG 73 :::
Qy	74	ACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGCCACC 112
дβ	25	PValProPhePheArgArgLysAspLysValValPheValMetGlyAlaThrGlyThr 44
р У	113 45	GGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCT 172
B 5	173 65	GACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAG 232 :: ::: :::
ογ	w	NTCTGCCGGCACATGATCAGCTTTTGTGGATCCTCTTTGTGACCAATTACACA
В	œ	::::::
γ	293	AGACAA
Дb	105	AlaGluAspPheGlnArgGluAlaIleArgAlaValGluSerIleValGlnArgAspArg 124
Qy	353	ATTCCTATTGTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTT 412

	i	i
	295 Lys	В
7 AGTTTCATC 1045	1037 AGT	Qy
5 GluGluAlaAspGluAlaTrpAspAsnSerValAlaHisProSerAlaLeuAlaValGlu 294	275 Glu	рь
	995	ç Qy
5 LysGlnTrpLysTrpAsnMetHisArgValAspAlaThrGluValPheLeuArgArgGly 274	255 Lys	дb
994		Qy
5 IleLysGluAsnThrCysLeuLeuAlaCysArgGlnLeuGlnLysIleGlnArgLeuTyr 254	235 Ile	дb
0 ATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAG 994	950 ATT	Qy
.5 GluMetArgAsnTyrProAlaGluThrThrGluArgLeuLeuGluThrAlaIleGluLys 234	215 Glu	Φb
	893 GAG	Qy
)5 TyrSerAlaGlyIleArgArgAlaIleGlyValProGluLeuAspGluPheLeuArgSer 214	195 Tyr	Db
	833 TAT	Qy
3 GluValArgArgIlePheAspProSerSerSerAsp 194	183 Glu	DЬ
GAACTAAGAGATTTTCACAGACGCTATAATCAG	773 GAA	Qy
	163 Val	Db
	713 GTT	Qy
	151	Дb
CTTGGAGGTCCTCTGAAGTTCTC	653 CTT	Qy
30 150	150	Db
3 ACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCC 652	593 ACA	Qy
30 150	150	Db
33 GCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAA 592	533 GCC	Qy
30 150	150	рь
3 GAAAAGGAGGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCT 532	473 GAA	Qy
11AsnAspCysValAspPheArgLeuArgTyr 150	141	DЬ
GTCAATACCAAGCCCCAGGAGATGGGCACT	413 GTC	Qy
25 ValProIleIleAlaGlyGlySerAsnSerTyrIleGluAlaLeuVal 140	125 Val	Db

Search completed: April 21, 2003, 18:55:40 Job time : 108.298 secs

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-DB-Públished_Applications_AA -OFMT-fastan -SUFFTX-n2p.rapb -MINMATCH-0.1
-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START=1 :END=-1 -WATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -CALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-USG9513151_@CGN_1_1_15_@runat_15042003_141145_26460
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG-DEV_TIMEOUT-120 -WARR_TIMEOUT-10 -THREADS-1 -XOAPOP-10 -XOAPEXT-0.5 -FGAPOP-6
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                                                                                                                                             Result
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-MODEL=frame+_n2p.model -DEV=xlh
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       1074
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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US-10-260-877-32
US-09-738-626-5633
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Sequence 586, App
Sequence 784, App
Sequence 32, Appl
Sequence 5633, Ap
                                                                                                                   Description
    Alignment Scores: Pred. No.:
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Sequence 8, Appli Sequence 6, Appli Sequence 62, Appli Sequence 5, Appli Sequence 14, Appl	equence 2, Appli quence 2, Appli quence 5, Appli quence 1444, A equence 4, Appli quence 5, Appli	equence 66, Applequence 7, Applequence 6988, A Sequence 5192, equence 13421, Sequence 13661, S	equence 43 equence 43 equence 43 equence 49 equence 2, equence 51 equence 51	

ALIGNMENTS

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NAME/KEY: SITE
COCATION: (124)
COTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (145)
COCATION: (145)
COTHER INFORMATION: X
US-09-764-853-586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-764-853-586
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 586
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 586, Application Patent No. US20020090672A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/764,853 CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                  Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                          TYPE: PRT
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an
FILE REFERENCE: 92706
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM o
NUMBER OF SED ID NOS: 939
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 784
LENGTH: 222
TYPE: PRT
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DB:
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Best Local Similarity:
                                                                                                                                                                                Sequence 784, Application Patent No. US20020090672A1 GENERAL INFORMATION:
 ORGANISM: Homo s
FEATURE:
NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATIC
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Sequence 32, Application US/10260877
Publication No. US/20030021813A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Chovan, Linda E.
APPLICANT: Hessler, Paul E.
APPLICANT: Hessler, Paul E.
APPLICANT: Reich, Karl A.
TITLE OF INVENTION: ESSENTIAL BACTERIA GENES ANI
TITLE OF INVENTION: USSENTIAL GENES'
FILE REFERENCE: 6565 US.P1
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Best Local Similarity:
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US-09-764-853-784
 CURRENT APPLICATION
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LOCATION: (145)
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NUMBER: US/10/260,877
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SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 32
LENGTH: 311
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PRIOR APPLICATION NUMBER: US/09/649,145
PRIOR FILING DATE: 2000-08-25
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Arg---GlyAspLeuAsnIleAsnLeuProSer-
                              CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA
                                                              GlnArgPheHisLysMetIleGluLeuGlyPheGlnAlaGluValGluLysLeuTyrAla
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 5633
LENGTH: 301
TYPE: PRT
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US-09-738-626-5633
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                                 TrpAsp---ValThrGluThrAlaSerValAlaArgPheGlnSerAspAlaValAlaAsp
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ATTGAATCTCTGCTC-----TGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGC
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-09-864-761-42725
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
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                                                       APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                                                                               APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                        APPLICATION NUMBER: US 60/234,687
                                                                                                 FILING DATE:
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Hanzel, David K.
Chen, Wensheng
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US-09-881-752A-230
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 230
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APPLICANT:
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/881,752A
                                                                                                          LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                           FILE REFERENCE: 06132/041002
                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020115078A1e1 H
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SOFTWARE: Annomax Sequence Listing
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D IN ADULT LIVER, SIGNA
D IN BT474, SIGNAL = 1.
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HIT: BE242161.1, EVALUE 3.00e-21
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Best Local Similarity:
Query Match:
DB:
                                                      ; ORGANISM: Homo sapiens US-09-759-508B-2
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US-09-759-508B-2
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                                                                                                                                                Sequence 2, Application US/09759508B
Publication No. US20020182599A1
GEMERAL INFORMATION:
APPLICANT: Fishman, Mark C.
TITLE OF INVENTION: Methods for Diagnosing and Treating Heart Disease
FILE REFERENCE: 00786/381002
CURRENT APPLICATION NUMBER: US/09/759,508B
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/175,787
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 11
                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENCTH: 26926
TYPE: PRT
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858	835 TCAACATGGTATCTTCCAATCAAT	Qy	
8265	245 uGluGluProPheValLeuProLeuThrGlnArgLeuSerIleAspAsnSerLysLysGl	Db 8	
834	AGAAGAATGTTTCGGAAAATAGCCAGGACTA	Qy	
8245	225 oGluGluIleLysLysArgAlaAlaProLeuValArgArgArgLysGlyGluValGlnGl	Db 49	
8225	212ProThrIleThrTrpIleLysAspGluAsnValIleValPr	Db 8	
720		Qy	
8211	::: 206 eSerGlySerProTyr	Db 8	
660	TCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGG	Q	
8206	:::	Db 8	
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240	шоливелольного вересостольного польшений вересостольного ве	9 9	
92	433 GATGGGCACTGAGAAAGTGACTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGT		
8148	128 gTrpLysArgCysAsnGluHisLeuValProIleLeuThrTyrThrAlaLysGlyLeuGl	Db 8	
432	AAGCCCCAGGA	Qy	
8128	108 rAspGlyGlySerLysIleMetGlyTyrIleIleGluLysIleAlaLysGlyGluGluAr	Db 8	
400	CCAATTATTACATTGAATCTCTGCTC	Qy	
363 8108	307 AAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGT :::	Qy Db 8	
8090	:::: ::: :::	Db 8	
306	стасатооттатала оставать в стастаста от том от	Ş	
246 8071	209	Qy Db 8	
8051	031 oValMetSerGlyGluAsnLysLeuSerTrpThrValLysAspLeuIleProAsnGlyGl	Db 8	
208	161 -ATCGTCAGGGCTGACTCCATGCAGGCTTATGAAGGCCTAGACATCATC	Qy	
8031	012 ThrProIleLeuHisTyrValLeuGluArgArgGluAlaGlyArgArg-ThrTyrIlePr	Db 8	
160	TGAG	Qy	
8011	001 LeuThrTrpGluProProGluPheAspGlyGly	Db 8	
108	CTACCTCTTGTAGTGATTCTCGGGGCCACGG	Qy	
8000	981 GlyLeuProGlyProCysLysAspIleLysAlaSerAspIleThrLysSerSerCysLys	Db 7	
48	ACGAGCAGTTCCTGTGGG	Оy	
	·513-151-3 (1-2041) x US-09-759-508B-2 (1-26926)	us-09-	
	rent Similarity: 33.21% Conservative: 67 : Local Similarity: 20.49% Mismatches: 183 :y Match: 169 y Match: 169 Gaps: 25	er er	
	116.00 Matches:	Score:	

Alignment Scores: 0.0477 Length: 628 Fred. No.: 115.00 Matches: 101 Percent Similarity: 34.39% Conservative: 83 Best Local Similarity: 18.88% Mismatches: 169	; TYPE: PKT ORGANISM: Physcomitrella patens US-09-828-447-12			P Z Z Z	BOHNERT, HANS VAN THIELEN, N CHEN, ROUYING ISHITANI, MANA	Sequence 12, Application US/09828447 Patent No. US20020069432A1 PATENT NORMATION: APPLICANT COSTA F STIVA OSWALDO DA	Db 8429 oLysAspAsnGlySerPro 8435 RESULT 8 IIS-09-928-447-12	OY 1282 TAAAGGGAAGGGATCCCCA 1300		Db 8390 oProCysValSerLysProLeuValAlaLysAspProPheGlyProProAspAlaProAs 8410 Ov 1222 CTCAGATGCTGTCAACACCATAGAAAAGTCAGAGTGTTTCCCCAGACTATAACAAAGAACC 1281	ор 6370 интекникуруютитутьенгиемтфунацияналимянатфунацургоктург 8390 Оу 1220GA 1221	1172 -ATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGAAGAAGATTG	Qy 1153 TCGCGAARGGGCAGCG	8350As	1093 AGCTGAGAACAAGAAGTTATCACCTGTGTGACCTCTGTGATCGAATCATCATTGGGGA	QY 1033 GCAAAGTTTCATCCAGGGGCCAČAAGCCTACAGCCACTCCAATAAAGATGCCATACAATGA 1092	Db 8317 gLysThrSerValLeuCysLysTrpGluProProLeuAspAspGlyGlySerGluIleIl 8337	973 AGAGGTATCTGAAGTCTGGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAATCGT	8302 uAspThr	Db 8284IleLysValGluAsnAspHisGlyIleAlaLysAlaProCysThrValSerValLe 8302	859 TGGC	::: Db 8265 yGluSerGlnLeuArgValArgAspSerLeuArgProAspHisGlyLeuTyrMet 8283
Qy 839 CATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAG 895	812	Qy 803 CAGAAGAAT	Qy 743 GATGACATGCTTGCTGGGCTCTTGGAGGGAACTAAGAGATTTTCACAGACGCTATAAT 802 :::::: :::: ::: Db 383 SerGluSerLysLeuGluLysValValGluLysTrpProGluAlaLeuValLysPheThr 402	Qy 704 GACCAGGCAGTTCTAGATGAGGGCTTTGGATAAGAGGGTG 742 ::::::	Qy 656 GGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCT 703	Qy 596 GGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTT 655 :::::::::::	Qy 536 AAGCTGCATCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACA 595 :::::: Db 304 GluValGluValLeuSerGlnLysGluMetSerThrProAlaGluLeuAsnSerArgSer 323	Db 284 ThrPheAlaProLeuGluGluAsnHisIleLeuGlyGluAsnThrProSerLeuArgLys 303	497CACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCC	Qy 467 496 Oy 467	Qy 407 GITCITGICANIACCAGGCCCCAGGAGATIGGCACTGAGAAAGIGAGCGAAAAGIG 400 ::::::::::::: ::: Db 244 IleIleIleSerThrLysProProLysGluTyrLeuGluAlaCysSerThrGlnLysLeu 263	224	Db 213 IleLeuGluGlnIle	CTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGGGGGAACCAATTAT	198 IleGluAspHisLeuThrSerGluLeuGlnGlyHisAlaAlaGlu	Db 182 IleLysAsnAlaPhePheThrSerGluTyrProValCysValThr 197	OY 230GAGCAGAGAATCTGCCGGCACCACATGATCAGC 262	::: :::	185 GTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAA	Qy 146 CGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAG 184		Query Match: 3.22% Indels: 182 DB: 10 Gaps: 26

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Patent NO. US20020146776A1
GENERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT
TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.515C2
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/007,693
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 157
SEQ ID NO 109
LENGTH: 867
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuAlaGluLeuLeuPheAsnLysGluGluAlaMetIleArgPheAspMetThrGluTyr 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlyValPheLeuPheLeuGlyProThrGlyValGlyLysThrGluLeuAlaLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAG
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Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T
Xu, H. Howard
                                                                                                                              Haselbeck, Robert
                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
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ThrMetAlaLysAsp

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-GGCCTAGACATCATCACC

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505 163	TTCACAAACGC laGlyLeuAsn	ACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACT 	5GA 4 TyrPheAsnAs	Qy 45 Db 14
454 143	ATT leThrValProAla	GAGATGGGCACTGAGAAAGTG 	5 CCCCAG-	Oy 42 Db 12
424 123	AATACCAAG LysLeuLys	.TTGAATCTCTGCTCTGGAAA ::: :: roGlnGluIleSerAlaLys	5 GTGGGAGGAACCAATTATTACA ::: { 4 IleSerGlyLysIleTyrThrP	Qу 36 рь 10
364 103	TT	TTGAAGATATATTTGCCCGA	5 AGAAATAGAGCAACTGCTC 	оу зо вь 9
304 95	ACAGTGGTGGACTTC ::: LysIleValAsp	luAlaGluLysArgLeuPro	.87TAC 77 PheAsnGluAspLysAlaLysGluAlaGluLysArgLeuProTyr	Qy 28 Db 7
76	IleMetGlyLeuMet	IleLys	/2 CCTCTTGTGACCAAT	Db 5
271 56	luSerAlaLysArg	T pLysGlyGluIleLeuVal	8 CACCACATGATCAGCTTTGTG :::::::: 7 ProSerIleValAlaPheThr	24
247 36		ATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGG TleIleAlaAsnLysGluGlyLysAsnThrThr	4 GGCCTAGACATCATC	Oy 19 Db 2
193 20	ATGCAGGTCTATGAA 1laMetAlaValTyrGlu	AGATCGTCAGCGCTGACTCC::::::::::::::::::::	37 CTAGGCCÀGCGGCTCGGCGGTGAGATCGTCAGCGGCTGACTCCATGCAGGTCTATGAA ::: ::: ::: ::: ::::: 1 MetGlyLysVallleGlyIleAspLeuGlyThrThrAsnSerAlaMetAlaValTyrGlu	Оу 13 Db
	0)	-815-242-11472 (1-620	13-151-3 (1-2041) x US-09	US-09-51
	620 107 75 768 203	Length: Matches: Conservative: Mismatches: Indels: Gaps:	nt Scores: 0.307 0.: 106.50 Similarity: 32.91% cal Similarity: 19.35% atch: 2.98%	Alignment Pred. No. Score: Percent S: Best Loca Query Matt DB:
		S I G	PRIOR FILING DATE: 2001-02-16 NUMBER OF SEQ ID NOS: 14110 SOFTWARE: FastSEQ for Windows SEQ ID NO 11472 LENGTH: 620 TYPE: PRT ORGANISM: Helicobacter pylor -09-815-242-11472	PRIOR NUMBE SOFTW SEQ ID LENG TYPE ORGA US-09-81
		,253,625 ,257,931 ,269,308	R APPLICATION NUMBER: 60/25: R FILING DATE: 2000-11-27 R FILING DATE: 2000-12-27 R FILING DATE: 2000-12-22 R FILING DATE: 2000-12-26 R APPLICATION NUMBER: 60/26	PRIOR PRIOR PRIOR PRIOR PRIOR
		206,848 207,727 242,578	R APPLICATION NUMBER: 60, R FILING DATE: 2000-05-23 R APPLICATION NUMBER: 60, R FILING DATE: 2000-05-26 R APPLICATION NUMBER: 60, B FILING DATE: 50,0-10-23	PRIOR PRIOR PRIOR PRIOR PRIOR
		200 01 SSERICIAL 5/09/815,242 -21 191,078	OF INVENTION: OF INVENTION: OF INVENTION: TO FILING DATE: APPLICATION NU FILING DATE: 2	FILE RE CURRENT CURRENT CURRENT PRIOR A PRIOR F
	Genes in	of Essential	E OF INVENTION: Identification	· PITLE

	GGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAA 1324	1286	Оу
494	hrValSerAlaGlnAspLysAsnThrGlyLysSerGlnGluIle	475	Db
1285	ATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACTATAACAAAGAACCTAAA	1226	Qy
474	Ala	455	рь
1225	-	1196	Оy
454	ln	435	Db
1195	ACATAAAATCCAAATCCCACTTGAAC	1142	Qy
434	AsnGlnProAlavalSerIleMetVal	419	Db
1141	ACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGTGATCGAATC	1082	Qy
418	ysValIleAspArgGlyThrThrIleProAlaLysLysSerGln	399	Db
1081	CTACAGCCACTCCA	1052	Qy
398	LysAspValLeuLeuLeuAspValThrPr	379	Db
1051		1051	Оу
378	ValAsnProAspGluValValAlaValGlyAlaSerIleGlnGlyGlyValLeuLysGly	359	Дb
1051	(,)	1007	Qy
358	ArgIleProLysValGlnGluArgValLysAlaPheIleAsnLysGluLeuAsnLysSer	339	Db
1006	TGGGAGGAGTCT	950	Qy
338	lyLeuThrLysAsnGluIleSe	319	Db
949	CTAAAGAAAGGACCTGGTCCC	914	Qy
318	erLeuThrGluAspLeuValGluGluThrIleSerLysIleGluSerValIle	299	Db.
913	TTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAG	863	Qy
298	${\tt PheIleThrAlaAspAlaThrGlyProLysHisLeuValLysLysLeuThrArgAlaLys}$	279	Db
862	ATTGGC	857	Оу
278	AlaAlaGluAsnAlaLysLysGluLeuSerSerAlaMetGluThrGluIleAsnLeuPro	259	Db
856	GTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAATCA	812	Оу
258	uThrGlyIleGluIleLysAsnAspValMetAlaLeuGlnArgLeuLysGlu	239	Db
811		767	Qy
238	AspaspPheAspAsnArgValIleAspPheLeuAlaAlaGluPhe	224	Дb
766	CAGGCAGTTCTAGATGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCT	707	Qy
223	AlaPheLeuGlyGly·····	219	Db
706	GGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGAC	647	Оу
218	LeuGluThrGlyAspAsnValValGluValLeuAlaThrGlyGlyAsp	203	Db
646	GAAACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGT	590	Qy
202	PheAspValThrVal	183	Db
589	AAAGTGGCCAGGAGCTTGCAAGTTTTTGAA	560	Qy
182	ValLeuArgIleIleAsnGluProThrSerAlaAlaLeuAlaTyrGlyLeuAspLys	164	망
559	-GACCCAGAAATGGCTGCCAAGCTGCATCCACATGACAAACGC	506	Qy

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APPLICANT: BARNWELL, JOHN
APPLICANT: MENDIS, KAMINI
FITLE OF INVENTION: RECOMBINANT PROTEIN CONTAINING A CITILE OF INVENTION: PLASMODIUM MSP-1
FILE REFERENCE: 0660-0135-0XCIP
CURRENT APPLICATION NUMBER: US/09/134,333
CURRENT FILING DATE: 1999-04-18
EARLIER APPLICATION NUMBER: PCT/FR97/00290
EARLIER FILING DATE: 1997-02-14
EARLIER APPLICATION NUMBER: FR96/01822
EARLIER FILING DATE: 1996-02-14
SOCTWARRE: PATCHING DATE: 1996-02-14
NUMBER OF SEQ ID NO 11
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LENGTH: 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09134333 Patent No. US20020076403A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROTH, CHARLES APPLICANT: NATO, FARIDABANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LONGACRE-ANDRE, SHIRLEY
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ORGANISM: Plasmodium cynomolgi
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                                       GlyAlaSerValAspLysAspMetValThrAlaAsnAspGlyLeuAlaTyrTyrGlnLys 130
                                                                                                                                                           CTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATT 454
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                                                                                                                                                                                                                                                                                                                                                           ProLeuAlaGlyMetTyrLysThrIleLysLysProLeuGluAsnHisValAsnAlaLeu
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                                                                              GACCGAAAAGTGGAG · ·
                                                                                                                 AspProTyrLysLeuLeuAspLeuGluLysLysLysLeuLeuGlySerTyrLysTyrIle
                                                                                                                                                                                                ValLeuAsnSerAspLeuAsnProTyrSerIleProHisSerGlyGluTyrIleIleLys
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Indels:
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Matches:
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               Query Match:
                                                                 Score:
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                                                                                                 Alignment Scores
                                                                                                                                   US-09-792-630-41
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Li, Min
APPLICANT: Dahiyat, Bassil I.
APPLICANT: Dahiyat, Bassil I.
EXECUTE: DATE: BIOCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES
TILE REFERENCE: A-70295/RFT/ENS/RMK
CURRENT APPLICATION NUMBER: US/09/792,630
CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                SEQ ID NO 41
LENGTH: 671
                                                                                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/09792630 Patent No. US20020168640A1
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                   SOFTWARE: PatentIn
                                                                                                                                            TYPE: PRT
ORGANISM: B19 virus
                                                                                 No.:
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                                                                                                         CATAGACAGGGGGACAATGGGACCAGGTCCTTTCTTTAGAAGCTGGTTACTAGTCTCCA 909
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                                                             rpLeuThrTrpCysAsnAlaGlnSerTrpAspHisTyrGluAsnTrpAlaIleAsnTyrT 483
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-151-3 (1-2041) x US-10-080-376-41 (1-671) TCACTCAAATCTAGAACTCCCAATATGTGGCTCACAAATACTTCAGTCATCTACAAAAGC 1740 ::: :::	US-09-513 Qy 1799	
nment Scores: 0.688 Length: 671 e: 103.00 Matches: 116 ent Similarity: 33.89% Conservative: 67 Local Similarity: 21.48% Mismatches: 170 y Match: 2.82% Indels: 187 g Gaps: 30	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	
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ESULT 13 S-10-080-376-41 S-quence 41, Application US/10080376 Patent No. US20020172968A1 GENERAL INFORMATION: APPLICANT: Li, Min APPLICANT: Dahiyat, Bassil I. APPLICANT: Dahiyat, BICCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES TITLE OF INVENTION: BICCHIPS COMPRISING NUCLEIC ACID/PROTEIN CONJUGATES FILE REFERENCE: A-70295-2/RTJ/RMS/RMK CURRENT APPLICATION NUMBER: NUMBE	RESULT 13 US-10-080- Sequence Patent N GENERAL APPLICA APPLICA TITLE O TITLE O CURRENT CURRENT	·
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GluAlaPheTyrThrProLeuAlaAspGlnPheArgGluLeuLeuValGlyValAspTyr 589	ОУ 566 Db 570	
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AGATACCATGTTGATAGTCCTGGCTATTTTTCCGAAACATTCTTCTGATTATAGCGTCTGT 789	Oy 848	
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	287	ThrSerThrPheLeuLeuHisThrAspPheGluGlnValMetCysIle	b 272	8
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1691 TTTAAAGGGATGCAGTCAATCCTGGTATTCACC 1659	1739 ATCTGGAAATTAGATAATTTTAGCCAGAGTCAGGGACATAAAACTTCT 1692	1799 TCACTCAAATCTAGAACTCCCAATATGTGGCTCACAAATACTTCAGTCATACAAAAGC 1740 ::: :::	09-513-151-3 (1-2041) x US-09-953-351-41 (1-671)	Alignment Scores: O.688 Pred. No.: O.688 Aches: O.688 Matches: Onservative: Best Local Similarity: Ouery Match: Ouery	TYPE: PRT ORGANISM: B19 virus -09-953-351-41	IOR FILING DATE: 2000-09-14 MBER OF SEQ ID NOS: 56 FTWARE: PatentIn version 3.1	FILE REFERENCE: A-70814/RFT/RMS/RMK CURRENT APPLICATION NUMBER: US/09/953,351 CURRENT FILING DATE: 2001-09-14 DRIDE APPLICATION NUMBER: IIS 60/232.960	APPLICANT: LIL, HOUSTAINS APPLICANT: Jin, Cheng He APPLICANT: Jin, Cheng He APPLICANT: AND COMPOSITIONS FOR THE CONSTRUCTION AND USE OF FU	H 5	14 953- ence	522 GlyAlaTrpTyrAsnGly	428 GGGGCTTGGTATTGACAAGAACTTTCCAGAGCAGAGATTCAATGTAATTAGTTGG 375	604HisIleAsnAsnSerGlyGlyGlyLeuGlyLeuCysProHisCysIleAsnVal 621	479 CCTTTTCAAGCTCCACTTTTCGGTCAATCACTTTCTCAGTGCCCATCTCCT 429		539 GCTTGGCAGCCATTTCTGGGTCCACCTGGCTTAGGCGTTTGTGAAGTACAAGACCATCCT 480	570 GluAlaPheTyrThrProLeuAlaAspGlnPheArgGluLeuLeuValGlyValAspTyr 589	566CCACTTTGCGTTTGTCATGTGGATGCA 540	550 SerGlyGluSerPheValGlySerSerValSerSerGluValValAlaAlaSerTrpGlu 569	623 GATGGAGAAATTCACTATGAGAGATTCCTGTTTCTTCAAAAAACTTGCAAGCTCCTGG 567	37	683 AAGGGTTAGAGAACTTCAGAGGACCTCCAAGGGGACCACCACCTTCTTCCGTATGTTGAC 624	<pre>:: 522 luSerSerPhePheAsnLeuIleThrProGlyAlaTrpAsnThr 536</pre>	728 AGCGCTCATCTAGAACTGCCTGGTCAGCATGAAGCCAAAGGATGC 684	508SerIleSerSerSerGlyGlyGluSerSerGluGluLeuSerG 522

Qy	Оу	Qy Db	Db Oy	Db	Db Oy	Оy	рb	Qy	D Oy	DЬ	Qy Db	Qy	Db 5	S B	Qy	Db Qy	Db	Qy	Qy Db	Db Qq	P	Qy	Дb
728 AGCGCTCA	788 GAAAATCTCTTAGTTCCTCCAAGAGCCCAGCCAGCCAGCC	848 AGATACCATGTTGATAGTCCTGGCTATTTTCCGAAACATTCTTCTGATTATAGCGTCTGT 789 500 hrThrPro	908 GTGTGCATTTTCCCTCAGTGATCAGGTACTCGTGAAATTCCTTGAAGCCAATTGATTG	YOO CATAGACAGGGGGACAATGGGACCAGGTCCTTTCTTTAGAAGCTGGTTACTAGTCTCCA 909	GTTCAAGAACAGACTCCTCCCACTTCGAGACATCAGATACCTCTAAGC	1076 TTATTGGAGTGGCTGTAGGCTTGTGGCCCTGGATGAAACTTTGCACGATTTCAAGAGCAG 1017 :::		CACAGAGGTCACACAGGTGATAACTTCTCTTGTTCTCAGCTTCATTGTATGGCATCT 1	1172 TGTGCGCTGCGCATTCGCGATCCCCAATGATGATTCGAT 1134 :::	:::	361 nAspValAlaGlyLysSerLeuValValTrpAspGluGlyIleIle		342 AlaLysSerValProValTyrGly-MetValAsnTrpAsnAsnGluAsnPheProPheAs 361	le 3	CCTCCCTCGAACTGGATCCCCACCACCTTTCCAAAGGCCACTGGACATGTCT	1439 AGAATTCCGCATAGCACTCCTTTGCCCAGACTGGGAGACAAACATACC 1392 ::: ::: 317	311	1499. AGAACGTGAGACTTTAAAACCACATCAAAAGAAAATGGTGGGAGCTTTTCTGCTATGCAG 1440	1559 ATCATTTCCAGACACACACACACACAAGGAGCTGACAAGACCTGCTGTTTCTATTATAG 1500 :::::: :::::::::::::::::::::::::::	1598 TTAAGGTTCAAAGAAAAAAATGCTTTCCTGAACTAC 1560 	ThrSerThrPheLeuLeuHisThrAspPheGluGlnValMetCysIle	1658 ACAAAGAAGATCCTCATGTATAAAAATGTGGGAATCTGTGCTGCTTTTAATAATAGAACCT 1599	::: ::: 253 PheGlnIleGlnSerAlaLeuLysLeuAlaIleTyrLysAlaThrAsnLeuValPro 271
Qy 1658 ACAAGAAGATCCTCATGTATAAAAATGTGGAATCTGTGCTGCTTTTAATAATAGAACCT 1599	TITAL AND SUBATION OF THE TOTAL OF T	1739 ATCTGGAAATTAGATAATTTTAGCCAGAGTCAGGGACATAAAACTTCT 1739 ATCTGGAAATTAGATAATTTTAGCCAG		-09-513-	Percent Similarity: 33.89% Conservative: 67 Best Local Similarity: 21.48% Mismatches: 170 Ouery Match: 2.82% Indels: 187 DB: 9 Gaps: 30	No.: 0.688 Length:	: TYPE: PRT ; ORGANISM: B19 virus US-10-082-671-47	SEQ ID NO 47 LENGTH: 671	PRIOR FILINGIANE: 2001-02-22 PRIOR FILINGIANE: DATE: 2001-02-22 UNUMBER OF SEQ ID NOS: 58 SOPTWARE: DATE: 7 1	CURRENT APPLICATION NUMBER: US/10/082,671 ; CURRENT FILING DATE: 2002-05-17 · DRIOR ADDITATION NUMBER: 6/270, 781	: TITLE OF INVENTION: USE OF NUCLEIC ACID LIBRARIES TO CREATE TOXICOLOGICAL .; TITLE OF INVENTION: PROFILES ; FILE REFERENCE: XEN/OO1	; APPLICANT: DAHIYAT, BASSIL ; APPLICANT: LI, MIN	Sequence 47, Application US/10082671 Sequence 47, Application US/20030049647A1 CENTRAL INFORMATION	ESULT 15	Oy 428 GGGCTTGGTATTGACAAGAACTTTCCAGAGCAGAGATTCAATGTAATAATTGG 375	604HisIleAsnAsnSerGlyGlyLeuGlyLeuCysProHisCysIleAsnVal	Ov 479 CCTTTCAAGCTCCACTTTTCGGTCAATCACTTTCTCAGTGGCCCATCTCCT 429	539 GCTTGGCAGCCATTTCTGGGTCCACCTTGGCTTAGGCGTTTGTGAAGTACAAGACCATCCT	570 GlualaPheTyrThrProLeuAlaAspGlnP		623 GATGGAGAAATTCACTATGAGAGATTCCTGTTTCTTCAAAAACTTGCAAGCTCCTGG	Qy 683 AAGGGTTAGAGAACTTCAGAGGGACCTCCAAGGGGACCACCACCTTCTTCCGTATGTTGAC 624	522 luSerSerPhePheAsnLeuIleThrProGlyAlaTrpAsnThr

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624	3 AAGGGTTAGAGAACTTCAGAGGACCTCCAAGGGGACCACCACCTTCTTC	68	Qy
536	2 luSerSerPhePheAsnLeuIleThrProGlyAla	52	В
684	8 AGCGCTCATCTAGAACTGCCTGGTC	72	Qy
522	8GlyGlyGluSerSerGlu	50	Db
729	8 GAAAATCTCTTAGTTCCTCCAAGAGCCCAGCAGCAAGCATGTCATCCACCCTCTTATCC	78	Qy
507	0 hrThrProIlevalThrAspThr	50	рь
789	8 AGATACCATGTTGATAGTCCTGGCTATT	84	Qy
500	:: ::: 3 hrPheAspPheProGlyIle	48	рь
849	8 GTGTGCATTTTCCCTCAGTGATCAGGTACTCGTGAAATTCCTTGAAGCC	90	Qy
483		46	Db
909	8 CATAGACAGGGGGGACAATGGGACCAGGTCCTTTCTTTAGAAGCTGGTTACTAGTCTCC	96	Qy
463	3 nPheThrValArgCysSerProAspMetGl	44	D ₀
969	6 GTTCAAGAACAGACTCCTCCCACTTCGAGACATCAGATACCTCT	101	Qy
443		42	DЬ
1017	6 TTATTGGAGTGGCTGTAGGCTTGTGGCCCTGGATGAAACTTTGCACGA	107	Qy
425	8ValProValValIleThrSerAsnGlyAspIleThrPheValVal	40	ДЪ
1077	3 CACAGAGGTCACAGGTGATAACTTCTCTTGTTCTCAGCTTCATTGTATGG	113	νQ
407	l nProThrArgValAspGl	39	Db
1134	- GTGCGCTGCCCATTCGCGATCCC	117	Qy
391	7	37	Db
1173	2 CAGCATCTGAGTCCAATCTTCTTCTTTCTTCAGTTGGTTCAAGTGGGATTTGG	123	Qy
376	l nAspValAlaGlyL	36	Db
1233	TATAGTCTGGGGAAACACTCTGAC	127	Qy
361	2 AlaLysSerValProValTyrGly-MetValAsnTrpAsnAsnGluAsnPheProPh	34	Db
1277	4 AAACGCTGCATTTCAGCTCTTGATCATTCTGCCCTTGGGGATCCCTTCCCCTTTAGGTTC	133	Qy
341	8 G1	32	Db
1335	CCTGAACTGGATCCCCACCACCTTTCCAAAGGCCACTGGACATGTCTCT	139	Ωу
327	ThrLe	31	В
1392	ACTGGGAGACAAACAT	143	Qy
316	1LeuLysTrpIleAspLys	31	Вρ
1440	CACATCAAAAGAAAATGGTGGGAGCTTTTCTGCTATGCAG	149	οy
310	lyGlnHisVal	30	Ър
1500	TCATTTCCAGACACATCAGCCACACAAGGAGCTGACAAGACCTGCTGTTTCTATTATAG	155	Qy
304	8LysAspAsnLysIleValLysLeuLeuLeuCysGlnAsnTyrAspProLeu	28	Db
1560	8 TTAAGGTTCAAAGAAAAAAAAATGCTTTCCTGAACTAC	159	Qy

Search completed: April 21, 2003, 19:01:37 Job time : 91.4237 secs

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Command line parameters:

-MODEL-frame+_n2p.model -DEV=xlh
-Q-Cgn2_1/USPTO_Spool_VUS09513151/runat_15042003_141249_27326/app_query.fasta_1.2183
-O--Cgn2_1/USPTO_Spool_VUS09513151/runat_15042003_141249_27326/app_query.fasta_1.2183
-DB-Published_Applications_AA -QFMT-fastan -SUFFIX-olin2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-oligo
-TRANS=human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-quality -THR_MIN=1
-ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US09513151_@CGN_1_1 13 _@runat_15042003_141249_27326
-NCPU=6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -KGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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                                                                                                                               Description
Sequence 586, App
Sequence 784, App
Sequence 42725, A
Sequence 1444, Ap
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US-09-764-853-586
                           Alignment Scores:
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 586
LENGTH: 222
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATION: >
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                    NAME/KEY: SITE
LOCATION: (145)
OTHER INFORMATION:
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                          US-09-513-151-3 (1-2041) x US-09-764-853-784 (1-222)
                                                                     Query Match:
                                                                                 Best Local Similarity:
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                                                                                                 Percent Similarity:
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 784
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 784, Application US/09764853 Patent No. US20020090672A1
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PJZ06
                                                                                                                                                                                                                         LOCATION: (124)
OTHER INFORMATION:
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                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (145)
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LOCATION: (124)
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US-09-864-761-42725
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00664 PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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                                 APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
                                                                           APPLICATION NUMBER: PCT/US01/00661 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00665
APPLICATION NUMBER: US FILING DATE: 2000-09-21
                                                                                                                                 APPLICATION NUMBER: PCT/US01/00662
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Hanzel, David K.
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PRIOR APPLICATION NUMBER: US 09/608,408

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; NAME/KEY: VARIANT
; LOCATION: (1)
; OTHER INFORMATION: Wherein Xaa may be any one of Arg or Gly or Trp
US-09-867-550-1444
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Best Local Similarity:
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                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1444
LENGTH: 115
TYPE: PAT
OBCANTAL
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2001-05-30
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42725
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OTHER INFORMATION:
                                                                                                                                                           ORGANISM: Homo sapiens
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Conley, Pamela
Law, Debbie
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N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.98
N: EXPRESSED IN HOLAT LIVER, SIGNAL = 1.1
N: EXPRESSED IN HELA, SIGNAL = 1.4
N: EXPRESSED IN PLACENTA, SIGNAL = 1.2
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
N: EXPRESSED IN BRAIN, SIGNAL = 1.2
N: EXPRESSED IN BRAIN = 1.2
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ban, Fuad,
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RESULT 6
US-09-970-989-17
Sequence 17, Application US/09970989
; Patent No. US20020156262A1
; Patent No. US20020156262A1
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SEQ ID NO 482
LENGTH: 139
TYPE: PRT
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                                                     CURRENT APPLICATION NUMBER: US/09/970,989
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/215,252
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 08/618,651
PRIOR APPLICATION NUMBER: US 08/618,651
PRIOR FILING DATE: 1996-03-19
                                                                                                                                                                                  TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE FILE REFERENCE: 077319/0151
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TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cell
TITLE OF INVENTION: Thereby
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 17
                                      NUMBER OF SEQ ID NOS: 42
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RESULT 7
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CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C20
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16
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TYPE: PRT
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APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
                                                                                                                                                                        APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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                                                                                                                                                            APPLICATION NUMBER: 60/066770
                                                                      FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/083322
                            APPLICATION NUMBER: FILING DATE: 1998-09
                                                          FILING DATE: 1998-04-28
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Botstein, David
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art, Timothy A.
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ILING DATE: 1998-06-

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APPLICATION NUMBER: 60/089952 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19

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Best Local Similarity:
Query Match:
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/989,293A CURRENT FILING DATE: 2001-11-20
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                              FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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                                                                                                     APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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Williams, P. Mickey
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Stewart, Timothy A.
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NUMBER: 60/087607
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60/091633

APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02

FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07

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NUMBER: 60/091982

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APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25

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APPLICATION NUMBER: 60/090678

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APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER:

60/090863 60/090862

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OR APPLICATION NUMBER: 60/089538
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OR APPLICATION NUMBER: 60/089600
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APPLICATION NUMBER: 60/088742
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APPLICANT: Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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Gerritsen, Mary E
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Eaton, Dan L.
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Botstein, David
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APPLICATION NUMBER: 60/089532
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Best Local Similarity:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C69
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OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/062250
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Baker, Kevin P.
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Williams, P. Mickey
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Gerritsen, Mary E
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E: 1998-06-03
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APPLICATION NUMBER: 60/091633
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APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/091519
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APPLICATION NUMBER: 60/090862
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066311
PRIOR FILING DATE: 1997-11-13
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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                                  APPLICATION NUMBER: 60/087759 ETILING DATE: 1998-06-02 APPLICATION NUMBER: 60/087827 FILING DATE: 1998-06-03
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Baker, Kevin P.
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Godowski, Paul
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Stewart, Timothy A.
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Alignment Pred. No.: Query DB: Percent Similarity:
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PRIOR APPLICATION NUMBER: 60/049787
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Stewart, Timothy A.
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                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                           Gaps:
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TITLE OF INVENTION: Secreted and Transmembra
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065186
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US-09-993-687-156
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                                                                     RR APPLICATION NUMBER: 60/01

BR FILING DATE: 1998-06-02

RR APPLICATION NUMBER: 60/01

BR FILING DATE: 1998-06-03

BR APPLICATION NUMBER: 60/01
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R FILING DATE:
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R FILING DATE:
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
                                         APPLICATION NUMBER: 60/088025
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FILING DATE: 1997-11-24
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Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumas,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni, Nicholas F
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             : 1998-06-04
NUMBER: 60/
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            60/088026
                                                                      60/088021
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60/088029

NUMBER: 60/088030

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60/088033

PRIOR

FILING DATE: 1998-UD-1U APPLICATION NUMBER: 60/088742

LING DATE: 1998-06-10

APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/

60/088734

APPLICATION NUMBER:

60/088655

FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212

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                                            US-09-513-151-3 (1-2041) x US-09-993-687-156 (1-378)
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Query Match:
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OR APPLICATION NUMBER: 60/09057
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PR APPLICATION NUMBER: 60/091978

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APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091478
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APPLICATION NUMBER: 60/090862
FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/090431
EILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090435
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FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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PRIOR

APPLICATION NUMBER:

1998-06-17

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APPLICATION NUMBER:

LING DATE:

1998-06-17

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FILING DATE:

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APPLICATION NUMBER: 60/089947

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60/089514

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APPLICATION NUMBER: 60/088876

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CATION NUMBER: 60/088861

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1998-06-16 1998-06-16 1998-06-12 1998-06-11 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-11 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-10

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RESULT 15
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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R FILING DATE: 1998-05-
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APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088025
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087759
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/
FILING DATE: 1997-10-17
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Roy, Margaret Ann
Stewart, Timothy
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Godowski, Paul J
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Gerritsen, Mary E.
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Ferrara, Napoleone
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b. US20030003531A1
             NUMBER: 60/088028
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DR APPLICATION NUMBER: 60/091633

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DR APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

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Search completed: April 21, 2003, 19:34:14
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/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/ECTUS_PUBCOMB.seq:*
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US-09-822-846-301
US-09-816-095-3
US-09-910-943-192
US-10-125-540-582
US-09-764-853-857
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Sequence 364, App
Sequence 4310, Ap
Sequence 10050, A
Sequence 26692, A
Sequence 9, Appli
Sequence 2777, Ap
Sequence 2780, Ap
Sequence 301, App
Sequence 192, App
Sequence 582, App
Sequence 582, App
Sequence 687, App
Sequence 1035, App
Sequence 214, App
Sequence 581, App
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	7		Sequence 6, Appli		Sequence 25, Appl	Sequence 17, Appl	Sequence 2035, Ap	Sequence 2035, Ap	Sequence 2034, Ap	Sequence 2034, Ap	Sequence 1986, Ap	Sequence 1986, Ap	Sequence 60, Appl	Sequence 24, Appl	Seguence 24, Appl	Seguence 24, Appl	Sequence 52, Appl	Sequence 59, Appl	Sequence 5442, Ap	Sequence 206, App	Sequence 1, Appli	Sequence 3814, Ap	Sequence 3, Appli	Sequence 490, App	Sequence 1034, Ap	Sequence 856, App

ALIGNMENTS

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OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (713)
OTHER INFORMATION: n
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                                          Query Match
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Matches 573;
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                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 166
LENGTH: 717
TYPE: DNA
                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE: RAME/KEY: SITE LOCATION: (619) OTHER INFORMATION: n equation:
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LOCATION: (625)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (655)
OTHER INFORMATION: n
                                                                                                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                              NAME/KEY: SITE LOCATION: (673)
44 GTGGGCACTGGGCTCAGGGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCC 103
                                                         Similarity
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                                          Score 473; DB 10;
Pred. No. 3.3e-239;
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                                                                                                                                                                                                                                     SEQ ID NO 364
LENGTH: 717
                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                   FEATURE:
NAME/KEY: SITE
LOCATION: (619)
                                                                                                                                                                                                                       LENGTH: 71
TYPE: DNA
NAME/KEY: SITE LOCATION: (713) OTHER INFORMATION:
                                     NAME/KEY: SITE LOCATION: (673) OTHER INFORMATION:
                                                                           NAME/KEY: SITE LOCATION: (655) OTHER INFORMATION:
                                                                                                                 NAME/KEY: SITE LOCATION: (625) OTHER INFORMATION:
                                                                                                                                                                                                         ORGANISM: Homo sapiens
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APPLICANT: GAIGET, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
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                 FILING DATE: 2000-05-04
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NUMBER:
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Pred. No. 3
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.3e-239;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-796-692-4310
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                                                  CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
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LENGTH: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10050, Application US/09864761 Patent No. US20020048763A1
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PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR APPLICATION NUMBER: 60/223,378
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K
APPLICANT: Chen, Wensheng
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                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Aeomica-X-1
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               APPLICATION NUMBER: PCT
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Hanzel, David K.
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PCT/US01/00667
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Pred. No. 2.3e-157;
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OTHER INFORMATION: MAP TO AL033527.25

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BOLE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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LENGTH: 457
TYPE: DNA
GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFU

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                       Sequence 26692, Application US/09864761 Patent No. US20020048763A1
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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145; Conserv
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; pred. No. 5.3e-66;
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NUMBER: US 60/207,456

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RESULT 6
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US-09-864-761-26692
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN BUILT LIVER, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN BUT474, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: STELHUMAN HIT: BE242161.1, EVALUE 3.00e-72

OTHER INFORMATION: SWISSPROT HIT: 09KAC3, EVALUE 2.00e-03
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PRIOR
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NUMBER OF SEQ ID NOS: 49117
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                                                                                                 AGAAATAGAGCAACTGCT 322
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APPLICATION NUMBER: US 09/608,408
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FILING DATE: 2001-01-30
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                                                                                                                                                                                          CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC 304
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FILING DATE
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100.0%; Pred. No. 2.5e-62;
vative 0; Mismatches 0;
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US-09-764-877-2777/c; Sequence 2777, Application; Patent No. US20020147140A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 9
LENGTH: 180557
TYPE: DNA
ORGANISM: Human
                                                                                         GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005
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SEQ ID NO 6
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Best Local S
Matches 23
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Matches 23; Conserv
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Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031 SOFTWARE: PatentIn Ver. 2.0
                                                CURRENT APPLICATION NUMBER: US/09/764,877 CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: CALL I AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P02066US1/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR APPLICATION NUMBER: 60/245,872
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APPLICANT: Agoulnik, Alexander I.
APPLICANT: Zhu, Qichao
TITLE OF INVENTION: CAN I AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P02066US1/10024824
CURRENT FILING DATE: 2001-11-02
CURRENT FILING DATE: 2001-11-02
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TYPE: DNA
ORGANISM: Human
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NUMBER OF SEQ ID NOS: 14
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les 23; Conserv
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0.19;
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; ORGANISM: Homo sapiens US-09-764-877-2780
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SEQ ID NO 2780
LENGTH: 1398
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Best Local Similarity
Matches 22; Conserv
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Best Local Similarity
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LENGTH: 1118
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CURRENT FILING DATE: 2001-01-17
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                 CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
                                                   FILE REFERENCE: GIN 6400
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                                                                                     APPLICANT:
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CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
                                                                                                                                                        APPLICANT
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                                                               PPLICANT: Gulukota, Kamalakar
PPLICANT: Graham, James R.
PPLICANT: Genetics Institute, Inc.
PPLICANT: Genetics Institute, Inc.
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Clark, Hilary
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Treacy, Maurice
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                                                                                                                                   Resnick, Richard J.
                                                                                                                                                   Howes, Steven H.
                                                                                                                                                                      Fechtel, Kim
                                                                                                                                                                                                                                    Bowman, Michael R.
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                                                                                                                                                                                                                                                                                                                           Evans, Chery
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Pred. No.
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                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 192 LENGTH: 716
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Best Local
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CURRENT FILING DATE: 2001-03-26 
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                    FILE REFERENCE: 7529/1G148US1
CURRENT APPLICATION NUMBER: US/09/910,943
CURRENT FILING DATE: 2001-07-23
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APPLICANT: Altman, Curtis
TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                    NUMBER OF SEQ ID NOS:
NAME/KEY: misc_feature LOCATION: (1)..(716) OTHER INFORMATION: n may be a
                                                                                                                                                                                                                                                                                                                                                                                             43316 AAATTTACAAGAAAAAAAAA 43336
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TYPE: DNA
                                                                                      TYPE: DNA
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                                                    FEATURE:
                                                                   ORGANISM: Xenopus laevis
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21; Conservative
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RESULT 15
US-09-764-853-857/c
Sequence 857, Application US/09764853;
Patent No. US20020090672A1
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US-09-764-870-582
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US-10-125-540-582
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APPLICANT: Rosen et al.
APPLICANT: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 582, Application US/09764870 Patent No. US20020042386A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                  Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PTZ14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                    LENGTH: 1684
TYPE: DNA
ORGANISM: Homo sapiens
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TYPE: DNA
ORGANISM: Homo sapiens
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Local Similarity 100.0%; local Similarity 0; onservative 0;
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vative 0; Mismatches C
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939 SOFTMARE: PatentIn Ver. 2.0 SEQ ID NO 857 LENGTH: 1684 TYPE: DNA ORGANISM: Homo sapiens US-09-764-853-857
Search completed: April 22, 2003, 00:12:53 Job time : 678 secs
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                                                                                                             Query Match
Best Local Similarity 100.
Matches 20; Conservative
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CURRENT FILING DATE: 2001-01-17
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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/cgn2_6/ptodata/2/pna,
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8 US-10-170-235-40554
9 US-10-342-887-1692
9 US-10-342-887-1692
11 US-60-453-135-276
11 US-60-453-050-276
11 US-60-453-050-275
11 US-60-453-050-275
11 US-60-453-050-275
11 US-60-453-050-275
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12 US-09-532-3158-9514
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US-10-380-731-119
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Sequence 134, App Sequence 41124, Ap Sequence 40554, A Sequence 276, App Sequence 277, App Sequence 277, App Sequence 278, App Sequence 278, App Sequence 278, App Sequence 279, App Sequence 279, App Sequence 3471, App Sequence 3471, App Sequence 3511, App Sequence 9511, App Sequence 9511, App Sequence 9511, App Sequence 9508, App Sequence 9508, App Sequence 9509, App Sequence 9509, App Sequence 9515, App Sequ
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	6.8	6.8	7.1	7.1	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	8.4	8.5	8.8	8.8	8.9	9.3	9.4
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	Sequence 6661, Ap	Sequence 111181,	Seguence 9528, Ap	Sequence 1534, Ap	Sequence 9520, Ap	•	Sequence 18368, A	Sequence 18364, A	Sequence 18362, A	Sequence 18357, A	Sequence 18354, A	Sequence 18368, A	Sequence 18364, A	Sequence 18362, A	Sequence 18357, A	Sequence 18354, A	Seguence 9529, Ap	Sequence 109804,	Sequence 9503, Ap	Sequence 9510, Ap	Sequence 9523, Ap	Sequence 9500, Ap	Sequence 9518, Ap

ALIGNMENTS

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; LOCATION: (191)..(1426)
US-09-659-671A-134
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US-09-659-671A-134
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Asundi, Vinod
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhang, Jie
                                                                                                                                                                                                                                                                                                                                       SOFTWARE: pt_FL_genes Version 2.0
SEO ID NO 134
LENGTH: 2130
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                                                                                                                                                                 Query Match
Best Local Similarity
Matches 896; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 794
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                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
164 · GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCT
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                                                                                                ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
                                                   ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC 163
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Xue, Aidong J.
Yang, Yonghong
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                                                                                                                                                                   Conservative
                                                                                                                                                                 43.9%; Score 896; DB 100.0%; Pred. No. 0; tive 0; Mismatches
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                                                                                                                                                                                                   Length 2130;
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                                                                                                                                                                        Sequence 119, Application US/10380731 GENERAL INFORMATION:
                                                          SEQ ID NO 119
LENGTH: 2130
                                                                                                                                           APPLICANT: Hyseg, Inc
TITLE OF INVENTION: NO
FILE REFERENCE: 21272
                                                                             PRIOR APPLICATION NUMBER: 09/659,671
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEO ID NOS: 888
SOFTWARE: Custom
                                                                                                                        CURRENT APPLICATION NUMBER: US/10/380,731 CURRENT FILING DATE: 2003-03-14
NAME/KEY: CDS
LOCATION: (191)..(1426)
10-380-731-119
                             ORGANISM: Homo sapiens FEATURE:
                                                 TYPE: DNA
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US-10-170-235-41124

Sequence 41124, Application US/10170235

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig

TITLE OF INVENTION: TRANSCRIPTS, FOR:
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NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF FOR DETECTING EXPRESSION AND OTHER USES THERE

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CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 41124
LENGTH: 1271
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Best Local
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                                         CTAAAATTATCTAATTTCCAGATGCTTTTGTAGATGACTGAAGTATTTGTGAGCCACATA
                                                                                                                                    CCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGAGACATGTCCAGTGGCCTT
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                                                                                       GTGGTGAATACCAGGATTGACTGCATCCCTTT - AAAGAAGTTTTATGTCCCTGACTCTGG
                                                                                                    GTGGTGAATACCAGGATTGACTGCATCCCTTTAAAAGAAGTTTTATGTCCCTGACTCTGG
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TTGGGAGTTCTAGATTTGAGTGAATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAG
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US-10-170-235-41123
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Best Local Similarity 99.9
Matches 1085; Conservative
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CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 41123
LENGTH: 1719
TYPE: DNA
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TITLE OF INVENTION: KITS, SUCH AS
TITLE OF INVENTION: TRANSCRIPTS,
FILE REFERENCE: CL001380
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Pred. No. 0;
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CURRENT APPLICATION NUMBER: US/10/170,23
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 40554
LENGTH: 2119
TYPE: DNA
ORGANISM: HUMAN
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APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLE TITLE OF INVENTION: TRANSCRIPTS, FOR EFILE REFERENCE: CL001380
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Best Local Similarity
Matches 1085; Conserva
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RESULT 6
US-10-342-887-1692
; Sequence 1692, Application
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
UNMBER OF SEQ ID NOS: 2699
SEQ ID NO 1692
LENGTH: 1749
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TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
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                                        GTTCTATTAAAAAGCAGCACAGATTCCACATTTTTATACATGAGGATCTTCTTTGTGG
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Van de Vijver, Marc J.
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Linsley, Peter
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US-60-453-135-276

Sequence 276, Application US/60453135

SEQUENCE LINFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: IAKOUBOVA, Olga

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET

FILE REFERENCE: CL001456

CURRENT APPLICATION UMBER: US/60/453,135

CURRENT FILING DATE: 2003-03-10
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 276
LENGTH: 1271
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-135-276
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Pred. No. 1.4e-298;
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APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:
TITLE OF INVENTION: STENOSIS, METHODS OF DE:
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 1271
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-050-276
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                                         Score 622; DB 11;
Pred. No. 1.4e-298;
0; Mismatches 5;
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                                       GGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCRGAATTCTACAGAGAA
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RESULT 9
US-60-453-135-274
US-60-453-135-274
; Sequence 274, Application US/6; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele; APPLICANT: IAKOUBOVA, Olga; TITLE OF INVENTION: GENETIC PO

US/60453135

POLYMORPHISMS

ASSOCIATED

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; LENGTH: 1719
; TYPE: DAN
; ORGANISM: Homo sapiens
US-60-453-135-274
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Best Local Similarity
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CURRENT FILLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
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 GGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAATT
                        GGGCCATCTCCATTGAGATGAATTAAGTGAACCAAACTAGTTCTCCRGAATTCTACAGAGAA
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                                                                                   TGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAATGGCAGGAAA
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Pred. No. 1.4e-298;
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CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 274
LENGTH: 1719
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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AAAAGCTCCCACCATTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCTCTATAATAGAA 1510
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Pred. No. 1.4e-298;
0; Mismatches 5;
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Sequence 275, Application US/60453135

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WIT
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF I
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 2119
LENGTH: 2119
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Best Local Similarity 99.4%;
Matches 992; Conservative
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                                        TATTTTTATTGAAGTTTAAATAAAGAAAAAATTTACAA 2028
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AACAAAGAACCTAAAGAGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGC
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Pred. No. 1.4e-298;
0; Mismatches 5;
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; ORGANISM: HOMO
US-60-453-050-275
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CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 2119
                                                                                                                                                                                                                                                                                                 Sequence 275, Application US/60453050 GENERAL INFORMATION:
                                                                                                                                                                                                               APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND U.
FILE REFERENCE: CL001457
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Score 622; DB 11;
Pred. No. 1.4e-298;
0; Mismatches 5;
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RESULT 13
US-09-532-315B-3472
; Sequence 3472, Application
; GENERAL INFORMATION:

US/09532315B

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FILE REFERENCE: PULLUC CLF
CURRENT APPLICATION NUMBER: US/09/532,315
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 07/916,491
PRIOR FILING DATE: 1992-07-17
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 09/977,780
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR FILING DATE: 1993-08-03
PRIOR APPLICATION NUMBER: 08/196,364
PRIOR APPLICATION NUMBER: 08/282,991
PRIOR APPLICATION NUMBER: 08/282,991
PRIOR APPLICATION NUMBER: 08/438,571
PRIOR APPLICATION NUMBER: 08/438,571
PRIOR APPLICATION NUMBER: 08/438,571
PRIOR APPLICATION NUMBER: 08/19,873
PRIOR APPLICATION NUMBER: 08/19,873
PRIOR APPLICATION NUMBER: 08/19,873
PRIOR APPLICATION NUMBER: 08/19,973
PRIOR APPLICATION NUMBER: 08/19,973
PRIOR APPLICATION NUMBER: 08/19,973
PRIOR APPLICATION NUMBER: 08/137,951
PRIOR APPLICATION NUMBER: 08/138,991
PRIOR APPLI
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu01286535
US-09-532-315B-3472
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100.0%; Pred. No. 4.4e-190;
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SOFTWARE: PERL Program
SEQ ID NO 3471
LENGTH: 392
TYPE: DNA
OPPORTURE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/532,315B CURRENT FILING DATE: 2000-03-24
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OTHER INFORMATION: Incyte ID No: hu01253362
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                                                               TTGCGAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTCTATTGAGTTACAAATCT 1989
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Pred. No. 6.7e-123;
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; OTHER INFORMATION: Incyte ID No: hu00875621
US-09-532-315B-9521
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SOFTWARE: PEKL
SEQ ID NO 9521
FONGTH: 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Seilhamer, Jeffrey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/916,491 PRIOR FILING DATE: 1992-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING TRANSFERASES FILE REFERENCE: PD-1002 CIP CURRENT APPLICATION NUMBER: US/09/532,315B CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 42212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 08/137,951 PRIOR FILING DATE: 1993-10-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1993-08-03
PRIOR APPLICATION NUMBER: 09/008,119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 07/977,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/
PRIOR FILING DATE: 1994-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 08/179,873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1994-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
 269
                                                                                                                                                      149
                                     284 AATTACACAGTGGTGGACTTCAGAA 308
                                                                                             224 GCCCAAGAGCAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 ATATTTTATTGAAGTTTAA
                                                                                                                                                                                                                                                                 104 ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                             44 GTGGGCAGTGGGCTCAGGGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 265; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/438,571 FILING DATE: 1995-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1995-07-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1994-01-1 APPLICATION NUMBER: 08
AATTACACAGTGGTGGACTTCAGAA 293
                                                                                                                                                    GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCT
                                                                                                                                                                        GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAACAAGGTTTCT
                                                                                                                                                                                                                              ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
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                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 6.6e-121;
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Search completed: April 22, 2003, 00:01:33 Job time : 977 secs

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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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cgn2_6/ptcdata/1/pna/US095_COMB.seq:*
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cgn2_6/ptcdata/1/pna/US09B_COMB
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7_COMB.seq:*
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/ Cgn2_6/ptodata/1/pna/US6011_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6012_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6013_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6013_COMB.seq:
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/ Cgn2_6/ptodata/1/pna/US6013_COMB.seq:
/ Cgn2_6/ptodata/1/pna/US6012_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6008_COMB.seq:

/cgn2_6/ptodata/1/pna/US6009_COMB.seq:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length		DB	ID	Description
1	2041	100.0	2041	19	US-09-513-151-3	Sequence 3, Appli
2	939	46.0	2108	40	US-10-133-013-165	Sequence 165, App
ω	939	46.0	2129	سر	PCT-US02-07826-152	Sequence 152, App
4	939	46.0	2129	39	US-10-097-340-152	Sequence 152, App
υī	918	45.0	2109	76	US-60-324-185-33690	Sequence 33690, A
6	823	40.3	2129	سر	PCT-US02-07826-150	Sequence 150, App
7	823	40.3	2129	39	US-10-097-340-150	Sequence 150, App
œ	818	40.1	2101	61	US-60-172-360-26034	Sequence 26034, A
9	778	38.1	1183	29	US-09-757-028-874	Sequence 874, App
10	778	38.1	1183	42	US-10-222-911-874	Sequence 874, App
c 11	757	37.1	1041	16	US-09-205-070-8140	
c 12	757	37.1	1041	17	US-09-340-623-8140	Seguence 8140, Ap
c 13	757	37.1	1041	ω ω	US-09-898-888-8140	Sequence 8140, Ap
c 14	757	37.1	1041	ω u	US-09-898-888A-8140	Sequence 8140, Ap
15	751	36.8	1749	ب	PCT-US02-18947-1692	Sequence 1692, Ap
16	751	36.8	1749	41	US-10-172-118-1692	Sequence 1692, Ap
17	697	34.1	1223	28	US-09-705-256A-6006	Sequence 6006, Ap
18	697	34.1	1223	60	US-60-164-285-6006	Sequence 6006, Ap
c 19	696	34.1	1039	17	US-09-359-922-3465	Seguence 3465, Ap
c 20	696	34.1	1039	17	US-09-359-922-3465	Sequence 3465, Ap
c 21	696	34.1	1039	ω 4	US-09-919-002-3465	Sequence 3465, Ap

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US-09-513-151-3

Sequence 3, Application US/09513151

GENERAL INFORMATION:
APPLICANT: MCGILL UNIVERSITY
TITLE OF INVENTION: THE C. ELEGANS gro-1
NUMBER OF SEQUENCES: 62
                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/CA98/00803
FILING DATE: 20-AUG-1998
PRIOR APPLICATION DATA: APPLICATION NUMBER: CA 2,210,251
FILING DATE: 25-AUG-1997
ATTORNET/AGENT INFORMATION:
NAME: Ctt, France
                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATION
OPERATING SYSTEM: Win
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: SWABEY OGILVY RENAULT
STREET: 1981 MCG111 College Avenue -
                                                                                                                                        REGISTRATION NUMBER: 4166
REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 514 845-7126
TELEFAX: 514 288-8389
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
       MOLECULE TYPE:
                     LENGTH: 2041 base por TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 19
CITY: Mont
                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                     2041 base pairs
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     Genomic DNA
                                 single
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US-09-289-68-25904

US-09-32-782-20244

US-09-737-223-20244

US-09-918-995-20244

US-09-918-995-2024

US-09-93-397-25904

US-09-584-852-5059
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US-10-072-326-364
US-09-652-127-7656
US-09-652-124-7628
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PCT-US01-01349-166
PCT-US01-01349-364
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US-09-399-932-5314
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RESULT 3
PCT-US02-07826-152
; Sequence 152, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030PC
; FILE REFERENCE: MRI-030PC
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/3276,026
PRIOR APPLICATION NUMBER: 60/376,026
PRIOR APPLICATION NUMBER: 60/376,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Homo sapiens
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                                                                                             CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCAT
                                  GCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGGCAGAGAAT
                  GCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAAT
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Sequence 152, Application US/10097340
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Sebastian HOERSCH
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                                                                       APPLICANT:
            TITLE OF INVENTION: Nucleic Acid TITLE OF INVENTION: Assessment, FILE REFERENCE: MRI-030
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APPLICATION NUMBER: US/10/097,340
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                                                                                                                                                                                             Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                        Xumei ZHAO
Karen GLATT
                                                                                                                   Gordon B. MILLS
Robert C. BAST,
                                                                                          Rosemarie SCHMANDT
                                                                                                        Karen LU
                                                                                                                                                    Peter VEIBY
                                                                                                                                                                 Ami SEN
                                                                                                                                                                                 Peter OLANDT
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                              Prevention,
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PRIOR RAPPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR PELLING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR PELLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/321,732
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
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US-60-324-185-33690
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TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS US
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
FILE REFERENCE: GX-0019-1 P
CURRENT APPLICATION NUMBER: US/60/324,185
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 35862
SOFTMARE: PERL Program
SEQ ID NO 33690
LENCTH: 2109
                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 918
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                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure LOCATION: 2106
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CTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGC 321
                                                                                             CATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAG
                                                                                                                                         CCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGA 201
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-07826-150
                                                                      PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4
                                            SOFTWARE: Fasts
SOFTWARE: Fasts
SEQ ID NO 150
FRIGTH: 2129
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PCT-US02-07826-150
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                                                                                                                                                                                                                                                                             APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030PC
CURRENT APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
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Sequence 150, Application US/10097340
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Wanjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
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PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
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Best Local Similarity
Matches 823; Conserv
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LENGTH: 2129
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Robert C. BAST, Jr
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; Sequence 26034, Appl
; GENERAL INFORMATION:
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APPLICANT: Diep, Dinh
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Us
TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide F
FILE REFERENCE: GX-0007 P
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILLNG DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOFTWARE: PERL Program
SEQ ID NO 26034
LENGTH: 2101
TYPE: DNA
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Best Local Similarity
                                                                                                                                                                                                                                      Matches 1088;
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                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No:
FEATURE:
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LOCATION: 2098
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Sequence 874, Application US/09757028
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PM001
CURRENT FILLING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: US/09/757,028
CURRENT FILLING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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I TYPE: DNA
ORGANISM: Homo sapie:
FEATURE:
I NAME/KEY: SITE
LOCATION: (1172)
OTHER INFORMATION: n
NAME/KEY: SITE
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SEQ ID NO 874
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CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/757,028
PRIOR FILING DATE: 2001-01-9
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFTWARE: PATENTIA Ver. 2.0
SEQ ID NO 874
LENGTH: 1183
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ORGANISM: Homo sapiens
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Sequence 8140, Application US/09205070

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED F
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748
CURRENT APPLICATION NUMBER: US/09/205,070
CURRENT FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASTSEQ for Windows Version 3.0

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US-09-205-070-8140/c

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Sequence 8140, Application US/09340623
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED F
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20417-748CON1
CURRENT APPLICATION NUMBER: US/09/340,623
CURRENT FILING DATE: 1999-06-28
EARLIER APPLICATION NUMBER: US 09/205,070
EARLIER APPLICATION UMBER: US 09/205,070
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 1041
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US-09-898-888-8140/c
; Sequence 8140, Application US/09898888
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FR.
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/898,888
; CURRENT FILING DATE: 2001-07-03
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RESULT 14
US-09-898-888A-8140/c
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FR
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR APPLICATION NUMBER: US/09/35,070
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207

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Best Local
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SEQ ID NO 8140
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TYPE: DNA
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                 CCAAACTAGTTCTCGGAATTCTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACA
                                                 GTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTAC 1062
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Pred. No. 0;
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APPLICANT: ROSECTA Inpharmatics
TIFILE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1692
LENGTH: 1749
LENGTH: 1749
CRGANISM: HOMO Sapiens
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DATABASE ENTRY DATE: 2001-06-18
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Pred. No. 0;
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Search completed: April 21, 2003, 23:43:40 Job time: 5197 secs

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Minimum DB seq length: 0
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2041
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US-08-494-624-1

US-08-117-907-1

US-08-453-040-1

US-08-187-793-1
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US-09-222-177A-49
US-09-289-349-2
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US-08-484-595B-17
US-08-480-150A-17
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US-08-485-731-17
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US-08-485-718-10
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US-09-152-060-24
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Sequence 56, Appl
Sequence 56, Appl
Patent No. 5475086
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Sequence 2505
Sequence 24,
Sequence 1, A
Sequence 49,
Sequence 2, A
Sequence 215
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US-09-370-838-175	US-08-978-289-3	US-09-033-055A-2	US-08-651-155B-22	PCT-US95-17111A-100	US-08-450-673C-100	US-08-340-426D-100	US-08-454-557C-100	US-08-594-031-144	US-08-594-031-137	US-08-594-031-45	US-09-306-290-31	US-09-128-155-17	US-09-426-290-1	US-09-245-281-44	US-09-810-671-3	US-08-687-080-68	US-09-245-041-4
Sequence 175, App	Sequence 3, Appli	Sequence 2, Appli	Sequence 22, Appl	Sequence 100, App	•	Sequence 100, App	Sequence 100, App	Sequence 144, App	Sequence 137, App	Sequence 45, Appl	Sequence 31, Appl	Sequence 17, Appl	Sequence 1, Appli	Sequence 44, Appl	Sequence 3, Appli	Sequence 68, Appl	Sequence 4, Appli

ALIGNMENTS

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Sequence 79, Application US/08781891

Patent NO. 6090650

GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: OShima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS REI
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
                  δÃ
                                                                                                                                                     US-08-781-891-79
                                                                                                                                                                                        CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: NO. 6090620tenburg ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-781-891-79
                                                         Query Match 1.1%; Score 23; DB 3; Best Local Similarity 100.0%; Pred. No. 0.18; Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

COUNTRY: USA

ZET: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, \

CURRENT APPLICATION DATA:
2019 AAATTTACAAGAAAAAAAAAAA 2041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6300 Co
CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/01 FILING DATE: 27-DEC-1996
                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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                                                                                                                                                                        ธรร: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/781,891
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RESULT 2
US-09-791-211-3
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SEQ ID NO 3
LENGTH: 87543
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09791211 Patent No. 6448080
                                                                        NAME/KEY: unsure
LOCATION: 33095
OTHER INFORMATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTISENSE MODULATION OF WRN EXPRESSION
FILE REFERENCE: RTS-0205
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LOCATION: 31205
OTHER INFORMATION:
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LOCATION: 31206
OTHER INFORMATION:
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LOCATION: 12742
OTHER INFORMATION: unknown
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                                LOCATION: 33160
OTHER INFORMATION:
                                                            NAME/KEY: unsure
                                                                                                                              OTHER INFORMATION:
                                                                                                                                                                                                                                                                                            NAME/KEY: unsure LOCATION: 30140
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LOCATION: 30136
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LOCATION: 12605
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LOCATION: 11609
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                                                                                                                                            NAME/KEY: unsure
LOCATION: 31592
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LOCATION: 29980
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OCATION: 29979
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OCATION: 29370
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LOCATION: 46808
OTHER INFORMATION: UNAME/KEY: unsure
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LOCATION: 63390
OTHER INFORMATION: U
NAME/KEY: unsure
LOCATION: 66614
OTHER INFORMATION: U
NAME/KEY: unsure
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LOCATION: 68718
OTHER INFORMATION:
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LOCATION: 36816
OTHER INFORMATION: unknown
                                                                            LOCATION: 68733
OTHER INFORMATION:
NAME/KEY: unsure
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LOCATION: 59242
OTHER INFORMATION:
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LOCATION: 59215
OTHER INFORMATION: unknown
NAME/KEY: unsure
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LOCATION: 52786
OTHER INFORMATION: unknown
 OTHER
                                             LOCATION: 68739
OTHER INFORMATION:
                                                                                                                         NAME/KEY: unsure
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LOCATION: 68697
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 47291
OTHER INFORMATION: unknown
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 42164
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LOCATION: 53384
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INFORMATION: unknown
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                                                                                                                 ; OTHER INFORMATION: unknown ; OTHER INFORMATION: US-09-791-211-10
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CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 98444
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                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: 79198
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: unknown OTHER INFORMATION:
36142 AAATTTACAAGAAAAAAAAA 36122
                                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: 24962
CTHER INFORMATION: unknown
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                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: 65471
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: unsure
LOCATION: 64383
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 86336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure LOCATION: 79134
                                                                                                                                                             NAME/KEY: unsure LOCATION: 89049
                                                                                                                                                                                            OTHER INFORMATION: unknown
                                                                                                                                                                                                          NAME/KEY: unsure LOCATION: 87130
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure LOCATION: 65469
                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure LOCATION: 65468
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                            2019 AAATTTACAAGAAAAAAAAA 2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Andrew T. Watt
VENTION: ANTISENSE MODULATION OF WRN EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donna T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                          Conservative
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100.0%;
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Pred. No.
                                                                      Score 21; D; Pred. No. 1
                                                           0
                                                           Mismatches
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0.18;
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                                                                                    Length 98844;
                                                           Indels
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RESULT 5
US-09-152-060-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-134-001C-2505
                                                                  ; ORGANISM: Homo sapiens US-09-152-060-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6380370
GENERAL INFORMATION:
APPLICANT.
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SEQ ID NO 2505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity Matches 19; Conserv
                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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 Query Match
Best Local Similarity
Matches 19; Conserv
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                EARLIER
EARLIER
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FILE REFERENCE: PZ003P1.US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/068,368 EARLIER FILING DATE: 1997-12-19 NUMBER OF SEQ ID NOS: 118
                                                                                                                                                                                                                        EARLIER FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT
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TYPE: DNA
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                                                                                                     TYPE: DNA
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                                                                                                                     ENGTH:
                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/057,765 FILING DATE: 1997-09-05
                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-05
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/050,934
                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-0: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/040,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-09-1
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/US98/04858
                                                                                                                                                                                                                                                                                           PLICATION NUMBER: 60/048,189
LING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                        LING DATE: 1997-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING DATE:
0.9%; Score 19; ilarity 100.0%; Pred. No. Conservative 0; Mismatcl
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Pred. No.
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                     DB 4;
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RESULT 7
US-08-222-177A-49/c
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                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/08222177A Patent No. 5582979
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/422,869
CURRENT FILING DATE: 1999-10-21
EARLIER APPLICATION NUMBER: 60/134,175
EARLIER FILING DATE: 1999-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES FILE REFERENCE: ARCD:307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35847 GAAGCTGAGAACAAGAGAA 35829
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                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1091 GAAGCTGAGAACAAGAGAA 1109
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                       STREET: 8000 E
CITY: Madison
STATE: Wiscons
                                                                   CLASSIFICATION: 435
                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
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: OTANI, KENICHI
: HANIS, CRAIG L.
: BELL, GRAEME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COX, NANCY J.
                                                                                                                                                                                                                                                       Wisconsin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09422869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLONSKY, KENNETH S
                                                                                                                                                                                                                                                                                    BOOO Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                            Weber, James L.
VENTION: LENGTH POLYMORPHISMS IN
VENTION: (dC_dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No
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US-08-222-177A-49
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                                                                                                                                                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 09:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 293 base pairs
                                                                                                                                                                                                                                                                                                                                              PUBLICATION INFORMATION:
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ORIGINAL SOURCE:
                                                                                      TITLE:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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CLONE: Mfd122
                                                                                                                                                                                                                                     AUTHORS:
                                                                                                                                 AUTHORS: Weber, James L.
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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                                                                                                                         AUTHORS:
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                                                                                                                                                                                                                                                                                                                  AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
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IDENTIFICATION METHOD: experime
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                                                                                                                                                                                                                                                                                   AUTHORS:
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                                                                                                                                                                                                                                                                                                                             AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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                                                                                                                                                                                     JOURNAL:
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Mapping of human chromosome 5 microsatellite
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                                                                                                                                                                                                    polymorphisms
                             388-396
                                                                           Reaction
                                                                                      Abundant Class of Human DNA Polymorphisms Which Can Be Typed Using the Polymerase Chain
                                                                                                                       May, Paula E.
                                                         Am. J. Hum. Genet.
                                                                                                                                                                                     Genomics
                                                                                                                                                                                                                                                                 Xiao, H.
                                                                                                                                                                                                                                                                               Kwitek, A. E.
                                                                                                                                                                                                                                                                                                               Polymeropoulos, M. H.
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name=
/citation= ((1))
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                                                                                                                                                                                                                                                                                                                                                             /standard_name=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "PCR primer"
/citation= ([1])
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "PCR primer"
                                                                                                                                                                                                                                                                                                                                                             "Only
                                                                                                                                                                                                                                                                                                                                                           one strand sequenced
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Query Match Best Local Similarity

0.9%;

Score 18; Pred. No.

DB 1; 46;

Length 293;

Matches

18;

US-09-289-349-2/c

GENERAL INFORMATION: Sequence 2, Appli Patent No. 627757

APPLICANT: APPLICANT:

SEQ ID NO 2 LENGTH: 618

TYPE: DNA

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; OTHER INFORMATION: 3534377CT1 US-09-289-349-2
                                                                                                                                                                 Query Match
Best Local Similarity
"hehes 18; Conserve
                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-2195
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Best Local Similarity
Matches 18; Conserv
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SEQ ID NO 2195
LENGTH: 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/289,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yue, Henry
TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/064,964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2024 TACAAGAAAAAAAAAAA 2041
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                                                                                                                                        2008 AAATAAAGAAAAATTTA 2025
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                                                                                         AAATAAAGAAAAATTTA 227
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Pred. No.
                                                                                                                                                                                                               Score 18;
Pred. No.
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46;
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                                                                                               RESULT 11
US-08-484-158B-17
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                                                                                                                                                                                                                                                                                                                                                                                            US-08-484-993B-17
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
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Sequence 17, Application US/08484158B Patent No. 5976545
GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/08484993B Patent No. 5837497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/973,341 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/012,990 FILING DATE: 29-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                              1206 TGTCCCTGACTCTGGCTA 1223
                                                                                                                                                                                                                                              1702 TGTCCCTGACTCTGGCTA 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: 1
ANTI-SENSE: NO
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1993
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  Harris Ph.D., Jeffrey D.
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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E: Ovary
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Pred. No
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South Wac
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ker Drive
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PRIOR FILING DATE:

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Sequence 2195,

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RESULT 10 US-08-484-993B-17

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RESULT 12
US-08-484-596A-17
; Sequence 17, Application US/08484596A
; Patent No. 5981228
; GENERAL INFORMATION:
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                                                                                                                                                                   Matches
                                                                                                                                                                                                Query Match
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                        1206 TGTCCCTGACTCTGGCTA 1223
                                                                                                                                       1702 TGTCCCTGACTCTGGCTA 1719
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APPLICATION NUMBER: 08,
FILING DATE: 29-JAN-93
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                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/9: FILING DATE: 09-NOV-92 ATTORNEY/AGENT INFORMATION:
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STREET: Tilinof
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                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Clough, David W. REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                  CELL TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/149,223 FILING DATE: 09-NOV-93
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HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Felis domesticus
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18; Conserv
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312/474-0448
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26..1297
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Podolski, Joseph S
                                                                                                                                                                   Conservative
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100.0%; Pr
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                                                                         Sequence 17, Patent No. 5
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                                                            GENERAL INFORMATION:
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                                                                                                                                                              1206 TGTCCCTGACTCTGGCTA 1223
                                                                                                                                                                                       1702 TGTCCCTGACTCTGGCTA 1719
                               APPLICANT:
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                   APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Felis domesticus
DEVELOPMENTAL STAGE: Juven:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illino
                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Clough, David W
REGISTRATION NUMBER: :
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                                                                                                                                                                                                                    Local Similarity
es 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                        LOCATION:
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                                                                         7, Application US/08480150A 5989550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
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                Harris Ph.D., Jeffrey D.
Hsu, Kuang T.
Podolski, Joseph S.
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                                                                                                                                                                                                                    Conservative
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100.0%; Pr
0;

    Joseph S.
    Materials and Methods for Immunocontraception

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Tower, 233
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                                                                                                                                                                                                                                                                                                                                                                           Juvenile
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                                                                                                                                                                                                                                Score 18;
Pred. No.
                                                                                                                                                                                                                   Mismatches
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South Wacker
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46;
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ker Drive
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NUMBER OF SEQUENCES:

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US-08-458-731-17
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                                                                                                                    Sequence 17,
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Best Local Similarity
Matches 18; Conserv
                                                                                                Patent No. 6001599
                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 25-3856
NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  1206
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
TITLE OF INVENTION: Materials and Methods for Immunocontraception
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                1702 TGTCCCTGACTCTGGCTA 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: UJCC
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: HAPLOTYPE: Diploidy
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-NOV-1993 APPLICATION NUMBER: 08/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 07-JUI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
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                                                                                                                                                                                                 TGTCCCTGACTCTGGCTA 1223
                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
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                                                                                                                  Application US/08458731
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6300 Sears Tower,
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Juvenile
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US-08-149-223A-17
                                                                                                                                                         Sequence 17, Application US/08149223A
Patent No. 6027727
                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                      GENERAL INFORMATION:
APPLICANT: Harris Ph.D., Jeffrey D.
APPLICANT: Hsu, Kuang T.
APPLICANT: Podolski, Joseph S.
APPLICANT: Podolski, Joseph S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           1206 TGTCCCTGACTCTGGCTA 1223
                                                                                                                                                                                                                                                                                           1702 TGTCCCTGACTCTGGCTA 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
LENGTH: 1319 base pair
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APPLICATION NUMBER: 08/012,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: HAPLOTYPE: Diploidy TISSUE TYPE: Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 09-NOV-1993
 CITY:
                                                                             TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0%;
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TELEFAX: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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STREET: 63
               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
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                                ADDRESSEE:
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Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1319 base pairs
               6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                             Conservative
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26..1297
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SYSTEM: PC-DOS/MS-DOS
                                Marshall
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    Joseph S.
    Materials and Methods for Immunocontraception

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                            O'Toole,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,107
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               ole, Gerstein, Murray & Borun
233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No
                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                            DB 3;
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Search completed: April 21, 2003, 23:50:13 Job time : 393 secs
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; LOCATION: 26..1297
US-08-149-223A-17
                                                                                                                                                                      Query Match 0.9
Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 3174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
TELEFAX: 312/474-0448
TELES: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1319 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA: 4797,341
APPLICATION NUMBER: 07/973,341
EILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Felis dom
                                                                                                                             1702 TGTCCCTGACTCTGGCTA 1719
                                                                                     1206 TGTCCCTGACTCTGCCTA 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/149,223A
FILING DATE: 09-NOV-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Felis domesticus
DEVELOPMENTAL STAGE: Juveni
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
CELL TYPE: Occyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                      0.9%; Score 18; DB 3;
100.0%; Pred. No. 46;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Juvenile
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Perfect score:
Sequence:
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Maximum DB seq
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                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                       Score
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length: 2000000000
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2041
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43.9
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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                                              AAS41268
ABL68710
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                                                                                                                                                                   Description
                                                cDNA encoding nove
Kidney cancer rela
                                                                                                                  Human homologue of Novel human coding
                Human
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                                                                                    Human cDNA
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breast cell
foetal liver
                                  colon cancer
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Human transporter	ABN85746	24	35357	1.1	22	4 5
Human immune/haema	L	22	32376	1.1	22	44
la	95	23	19802	1.1	22	43
	ABL17248	23	6399	1.1	22	42
	64	23	6228	1.1	22	41
	ABL10424	23	6225	1.1	22	40
Human immune/haema	AAK66112	22	1398		22	39
Human musculoskele	AAL36415	22	1398	•	22	38
Human musculoskele	AAL36412	22	1118		22	37
Ω.	AAK78227	22	885		22	36
Human secreted pro	AAC26737	21	190	•	22	ა 5
ē	AAX83003	18	87350	1.1	23	34
Nucleotide sequenc	AAH24652	22	33780		23	ω ω
DNA encoding novel	AAS84109	23	15879	•	23	32
	AAS82685	23	13234		23	31
	AAS87396	23	11378	•	23	30
DNA encoding novel	AAS74637	23	11087		23	29
Human immune/haema	AAK87244	22	7488	٠	23	28
Human immune/haema	AAK87243	22	7488	•	23	27
DNA encoding novel	AAS81397	23	7313	1.1	23	26
Human polynucleoti	AAI92597	22	6881		23	25
DNA encoding novel	AAS79149	23	4557		23	24
DNA encoding novel	AAS88985	23	2001		23	23
te	ABV19646	23	545		40	22
Human prostate exp	ABV49413	23	582	2.9	59	21
Human spliced tran	ABN34729	24	60		60	20
used	AAI46014	22	138	•	w	19
Probe #10720 for g	9	22	138	•	w	18
bone m	999	22	138	٠	w	17
Human brain expres	426	22	138		w	16
Human foetal liver	585	22	138	•	w	15
Human breast cell	796	22	138	•	w	14
#1548 used	286	22	457	•	4	13
#1507	_	22	457	7.1	145	12
n bone m	969	22	457	7.1	4	11
Human brain expres	AAK01519	22	457	7.1	145	10

ALIGNMENTS

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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                     gro-1 operon; gro-1 gene; gop-1 gene; gop-2 gene; hap-1 gene; cancer; aging; longevity; tumour formation; physiological clock; ss.
Molecular identity of the gro-1 gene - useful for cancer diagnosis and/or prognosis, and where compounds affecting encoded proteins are \,
                                                                                                                                                                                                                                                                  04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human homologue of gro-1, referred to as hgro-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX36073;
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                                                               WPI; 1999-190615/16.
                                                                                                   Barnes T,
                                                                                                                                                                                                                                                                                                          W09910482-A1
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                    25-AUG-1997;
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                                                                                                                                         (UYMC-) UNIV MCGILL.
                                                                                                     Hekimi S,
                                                                                                                                                                                    97CA-2210251
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                                                                                                     Lakowski
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or prognosis of cancer in a patient. Transgenic mice containing a gene knock-out of a murine gene homologue of the gro-1 gene are useful as models of aging and cancer. The proteins encoded by the genes are useful for identifying compounds that affect the enzymatic activity of these proteins, in order to enhance longevity of a host and inhibit tumour formation. The gro-1 gene, together with the gop-1, gop-2, gop-3 and hap-1 genes enables study of a physiological clock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the human homologue of gro-1, and is referred to as hgro-1. The specification describes the five genes of the Caenorhabditis elegans gro-1 operon (AAX36071). The operon contains the gro-1 gene (AAX36072), the gop-1 gene (AAX36074), the gop-2 gene (AAX36075), the gop-2 gene (AAX36075), and the hap-1 gene (AAX36077). The gro-1 gene can be used in a method for the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
  661
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            TCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGA
                                                             CTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTGGTCCCCTTGGAGG
                                                                                                  GCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAAT
                                                                                                                                                      GGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCT
                                                                                                                                                                                                           TGTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATAC
                                                                                                                                                                                                                                                                                                                 CTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGG
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TCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGA
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Pred. No. 0;
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1860	TGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATT :	1801	Qy
1800	ATGACTGAAGTATTTGTGAGC	1741	дЬ
1800	TTTTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAA	1741	Qy
1740	CCCTTTAAAAGAAGTTTTATGTCCCTGACTCTGGCTAAAATTATCTAATTTCCAGATG	6	Db
1740	TTTCCAGATG	1681	Qy
83		Ġ	Дb
1680	CAGATTCCACATTTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGGATTGACTGC	1621	Qy
1620	TTTTCTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGC	5	Db
1620	AGTTCAGGAAAGCATTTTTTTTTTTTTTTGAACCTTAAAGGTTCTATTATTAAAAGC	1561	Qy
ō	TGTCAGCTCCTTGTGTC	ū	Дb
	ATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTGTGGCTGATGTGTCTGGAAATGAT	1501	Qy
ŏ .		4.4	Db :
1500	GCATAGCAGAAAAGCTCCCACCATTTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCT	1441	ν
1440		1381	Db
1440	AGGAGGGAGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCT	w	Qγ
1380	GAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTT		Db
1380	AAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGT	1321	Qy
	CCCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCT	N	Дb
N	CCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCCAGGGCAGAATGATCAAGA	N	Qy
1260	GAAGATTGGACTCA	Ν	Db
1260	AAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGT	Ν	Qy
	ATCGCGAATGGGCA	1141	dd
1200	ATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAATTGGAACCAAC	\vdash	Qy
1140	AGCTGAGAACAAGAGAA	1081	DЬ
1140	GCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGAGCCTCTGTGATCGAA	Ö	9
1080	TCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTC	0	οь
1080	CTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGA	0	Qy
02	TCTCGAAGTGGGAGGAGTCTGTTC	961	Дb
1020	GTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTG	961	Q V
960	TAACCAGCTTCTAAAGAAAGG?	901	Ф
960	TGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCC	901	Qу
900	TGGTATCTTCCAATTCAATTGGCTTCAAGGAATTTCACGAGTAC	841	Db
900	GGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAA	841	Оy
840			Db
840	GATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAAC	781	Qy
780	TGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTTGGAGGAACTAAG	721	Db
780	GAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTTGGAGGAACTA	721	Qy

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RESULT 2
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                            The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                          Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
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Sequence
                                                                                                                                                    Claim 1;
                                                                                                                                                                         An isolated polynucleotide for treating diseases encoded polypeptide such as cancer and multiple s
                                                                                                                                                                                                          WPI; 2002-292408/33.
P-PSDB; ABB97295.
                                                                                                                                                                                                                                                                                               11-SEP-2000; 2000US-0659671
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                                                                                                                                                                                                                                                                                                                                                                                                         expressed sequence
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                                                                                                                                                                                                                                         Liu
Yang
 2130
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Query Match

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ABA06500
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Human cDNA 10-JAN-2002

SEQ

NO: 166

(first entry) IJ

RESULT

ABA06500

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                                     AGCCAGGACTATCAACATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTAC
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08-SEP-2000; 2000U 08-SEP-2000; 2000U 08-SEP-2000; 2000U 08-SEP-2000; 2000U 12-SEP-2000; 2000U 14-SEP-2000; 2000U	PX XX XX	XX KW Human; gene therapy; neural disorder; immune KW muscular disorder; reproductive disorder; ga: KW pulmonary disorder; cardiovascular disorder; KW proliferative disorder; inflammation; ss. XX XX OS Homo sapiens. XX PN W0200154474-A2.
		<pre>Immune system disorder; ar; gastrointestinal disorder; order; renal disorder; ss.</pre>
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                                                                                                                                                                                                                                                                                                                                                                             he present invention provides human cDNAs, proteins and related genomic NAs. These can be used in the treatment of neural, immune system, iscular, reproductive, gastrointestinal, pulmonary, cardiovascular, and proliferative disorders and inflammation. The present sequence a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity es 573; Conserv
                                                                                                                                                                                                                                                                GCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACC
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DB; ABB10278.
                                    TTTGAAGAAACAGGAATCTCTCATAGTGAATTTCT
                                                                        GAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTT
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2001US-259678P.
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07-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 717 BP; 184 A; 177 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO: 364; 859pp + Sequence Listing; English.
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P-PSDB; ABB10476.
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               CGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                   ACGGCACCGGCAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
                                                                                                                                                  AAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAA
                                                                                                                                                                                                                                                                                  AATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCC
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                                                                                                                                                                                                                                                                                                                                                      GCCCAAGAGCAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACC
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2000US-251988P.
2000US-251479P.
2000US-251868P.
2000US-251869P.
2000US-251869P.
2000US-251989P.
2000US-251989P.
2000US-251989P.
2000US-251989P.
2000US-2599P.
2000US-2599P.
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Pred. No. 1.3e-213;
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G; 162 T; 7 other;

Length Indels

0

Gaps

0

403

343 343 283

283

223 163 163 103 103

223

523 523 463 463 403

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RESULT 5
AAS41268
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11-JUL-2000

11-JUL-2000

14-JUL-2000

26-JUL-2000

26-JUL-2000

14-AUG-2000

15-AUG-2000

22-AUG-2000

23-AUG-2000

21-AUG-2000

21-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
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                 2000US-0180628.
2000US-0184664.
2000US-019676.
2000US-0199076.
2000US-02148867.
2000US-02148867.
2000US-02148867.
2000US-0214887.
2000US-02148867.
2000US-0214886.
2000US-0214886.
2000US-0214887.
2000US-02182964.
2000US-0225913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isomerase;
       06-SEP-2000
08-SEP-2000
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08-SEP-2000
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08-SEP-2000
14-SEP-2000
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29-SEP-2000
20-CCT-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
29-SEP-2000
20-CCT-2000
20-CCT
   2000US-0231244.
2000US-0231413.
2000US-0231414.
2000US-023208.
2000US-0232397.
2000US-0232397.
2000US-0232398.
2000US-02332401.
2000US-02332401.
2000US-0233421.
2000US-0234223.
2000US-023423.
2000US-023424.
2000US-023424.
2000US-023424.
2000US-0234297.
2000US-0235834.
2000US-0235834.
2000US-0235834.
2000US-0235834.
2000US-0235834.
2000US-0235834.
2000US-0235836.
2000US-0235836.
2000US-0236367.
2000US-0236367.
2000US-0241787.
2000US-0241787.
2000US-0241787.
2000US-0241787.
2000US-0244677.
2000US-0246477.
2000US-0246477.
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2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246611.
2000US-0246523.
2000US-0246611.
2000US-0246523.
2000US-0246611.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246523.
2000US-0246611.
2000US-0246523.
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2000US-0231242.
2000US-0231243.
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                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                           Query Match
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01-DEC-2000
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08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                   Sequence 717 BP;
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17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-NOV-2000;
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17-NOV-2000;
      164
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                                          164
                                                                                                                             104
                                                                                                                                                                   44
                                                                                                                                                                                       44 GTGGGCAGTGGGCTCAGGGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCC 103
                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                       GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAACAAGGTTTTCT
                                                                                                    ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
GTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCT
                                                                                ACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATC
                                                                                                                                                                 GTGGGCAGTGGGCTCAGGGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCC
                                                                                                                                                                                                                                                  573;
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                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000US-0249244
2000US-0249245;
2000US-0249265;
2000US-0249297;
2000US-0249297;
2000US-0249290,
2000US-0249300,
2000US-0250160,
2000US-0250160,
2000US-0251030,
2000US-0251988,
2000US-0251479,
2000US-0251866,
2000US-0251866,
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2000US-0254097.
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                                                                                                                                                                                                                                                                                                                               184 A; 177 C; 187 G; 162 T; 7 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               494; 1180pp; English
                                                                                                                                                                                                                                                                   23.2%;
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                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                            Score 473; DB 22;
Pred. No. 1.3e-213;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM.
                                                                                                                                                                                                                                                                                      Length
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RESULT 6
ABL68710/c
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22-SEP-2000
25-SEP-2000
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27-SEP-2000
                                                                                                                                                                      05-JUN-2000;
05-JUN-2000;
18-SEP-2000;
                                                                                                                                                                                                                                                                                          Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                    18-SEP-2000;
20-SEP-2000;
                                                                                                                                                                                                                                                                                                                                  Kidney cancer related gene sequence
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                                                                                                                                          20-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA;
                                            2000US-234924P
2000US-235077P
2000US-235082P
2000US-235134P
2000US-235280P
2000US-23537P
                                                                                                                                2000US-234009P.
2000US-234034P.
2000US-234052P.
        2000US-235720P
2000US-235840P
                           2000US-235638P
2000US-235711P
                                                                                                                                                                                                          2001WO-US10838
                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                     2000US-234567P.
2000US-234923P.
                                                                                                                                                                       2000US-209531P
2000US-233133P
                                                                                                                         2000US-234509P
                                                                                                                                                             2000US-233617P
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                                                                                                                                                                                                                                                                                          cc agent to be tested for anti-neoplastic activity, determining a change in comprises a sequence (5) selected from 8447 sequences (given in ABL6164 to ABL70110), or is at least 95% identical to (S), where a change in certivity and can be used in gene therapy. M1 can be used for screening an arti-neoplastic agent, and can be used for producting a product which is the data collected with respect to the anti-neoplastic agent as a cresult of M1, and the data is sufficient to convey the chemical consensually of cancer such as colon, breast, stomach, lung, thyroid, cossophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 341; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-SEP-2000

28-SEP-2000

28-SEP-2000

28-SEP-2000

28-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

02-OCT-2000

03-OCT-2000

03-OCT-2000
             1870
                                                                                                                                                    Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene
                                                                                                                                                                                                                                                                      Sequence 355 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method (MI) for screening for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-neoplastic agent. The method involves exposing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AVAL-) AVALON PHARM.
                                                                                                  283
AGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAAT
                                                                                                               ATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAATGGCAGGAA 1809
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                                         AGGCCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCAGAATTCTACAGAGA
                                                                    AGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATTCTACAGAGA
                                                                                                ATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAATGGCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Augustus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-237425P.
2000US-237598P.
2000US-237604P.
2000US-237606P.
2000US-237608P.
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                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID 7047; 44pp; English.
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2000US-245084P
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2000US-237294P
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2000US-236032P
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                                                                                                                                                                                                                            11.8%;
99.4%;
                                                                                                                                                                                                                                                                      A; 74 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carter
                                                                                                                                                                                                              0;
                                                                                                                                                                                                                            Score 241; DB 24;
Pred. No. 9.5e-104;
                                                                                                                                                                                                                                                                      54 G; 115 T; 0 other;
                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S,
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                                                                                                                                                                                                                                        Length 355;
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              1929
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RESULT 7
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ID AAA0
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                                                                  AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                                                                                                                                                                                                                                                                    Williams LT,
Reinhard C,
Lamson G, Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                        WPI;
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                         pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor positive breast cancer, oestrogen receptor
                                                                                                                                                                                                                                                                                           Claim 1; Page 399; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oestrogen receptor-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA00911 standard; cDNA; 300
              negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                           cells
                                                                                                                                                                                                                                                                                                                                         Polynucleotide library used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         Leshkowitz D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATATTTTATTGAAGTTTAAATAAAGAAAAATTTACAAGAAA 2032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colon cancer; tumour; diagnosis; gene expression product;
detection; cancerous state; metastasis; identification;
                                                                                                                                                                                                                                                                                                                                                                                                       C, Giese K,
Drmanac R,
z D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer cell line
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98US-0085696.
98US-0105234.
98US-0105877.
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Randazzo F, Ke
Crkvenjakov R,
, Garcia V, Jon
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                                                                                                                                                                                                                                                                                                                                         determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                      R, Garcia PD,
Kennedy GC, P
R, Dickson M,
                                                                                                                                                                                                                                                                                                                                                                                                         Jones LW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD,
                                                                                                                                                                                                                                                                                                                                                                                                         Stache-Crain
                                                                                                                                                                                                                                                                                                                                                                                                         Pot D, Kassam
1, Drmanac S, 1
ache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudduth-Klinger
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ABA42839/c
ID ABA428
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AC ABA428
AC ABA428
AXX
DE Human
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Human;
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PD 09-AUG
PF 30-JAN
XX
O9-AUG
PR 26-MAY
PR 30-JUN
PR 27-SEP
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gen
                                                                                                                   nucleic acid probes for measuring gene expression in a sample deri-
from human breast and BT 474 cells. The method involves contacting
the probes with a collection of detectably labelled nucleic acids
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                                                                                                                                                                                                                                                                                     New spatially-addressable set of single exon nucleic acid useful for measuring gene expression in sample derived frobreast, comprises number of single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
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                                                                                                                                                                                           The invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                             Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-496933/54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; microarray;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCTGGTCCCATTGTCCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGG 998
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225; Conserv
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236559.
2000US-0236559.
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                                                                                                                                                                                                                                        ID NO 1534; 327pp + sequence listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 175;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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.7e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe #1534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                          probes
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                                                                        for
     Gene
                                                                                                                                                                       derived
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RESULT 9
ABA53262/c
ID ABA53262
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agents on cells. The microarray of this invention presents a rar year agents on cells. The microarray of this invention presents a rar year diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                 Human; foetal liver;
                                                                                                                                   01-FEB-2002
                                                                                                                                                                    ABA53262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression analysis is useful for assessing the toxicity of chemical
WO200157277-A2
                                                                                                 Human foetal liver single exon nucleic acid probe #1567.
                                                                                                                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                         390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGAGCAGAGAAATCT
                                                                                                                                                                                                                                                                                                                        TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                         GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT
                                                                                                                                                                                                                                                                                                                                                                                         GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT
                                                                                                                                                                                                                                                                                        TCAGAAATAGAGCAACTGCTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGGTTTCTGCCCCAAGAGCAGAGAATCT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
145; Conserv
                                                                                                                                                                                                    standard;
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                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 A;
                                                                                                                                                                                                    DNA;
                                                                                                                                   entry
                                                               gene expression; single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102
                                                                                                                                                                                                      457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 145; DB 22; Pred. No. 2.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; 110 G; 125
                                                                                                                                                                                                                                                                                        306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 457;
                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              presents a far greater with far less bias
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                                                                 probe;
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                                                                   SS
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                              04-FEB-2000;
26-MAY-2000;
                                                                                                                    09-AUG-2001
                                                               (MOLE-)
                                                                                          30-JUN-2000;
                                                                                                            30-JAN-2001;
                                                        sc,
                                                                MOLECULAR DYNAMICS INC
                                                        Hanzel
                                                                        2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                              2000US-0180312.
2000US-0207456.
                                                                                                            2001WO-US00669
                                                       DK,
                                                        Chen
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measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid

The invention relates to a single exon nucleic acid

eic acid probe for derived from human

English.

analyzing

genome-derived single exon nucleic acid |
zing gene expression in human fetal liver

probes useful

for

2001-483447/52

Claim

SEQ

ID NO 1567; 639pp + sequence listing;

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RESULT 10
AAK01519/c
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밁
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 145;
                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human probes. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                    04-FEB-2000; 2000US-0180312; 26-MAY-2000; 2000US-0207456; 30-JUN-2000; 2000US-0608408; 03-AUG-2000; 2000US-0632366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                microarray; Alzheimer's disease; epilepsy; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe of the invention. Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                              Single
                                                                                                                                                                                                                                                            21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK01519 standard;
                                                                                                                                                                        WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                   WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID
                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression
            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCAGAAATAGAGCAACTGCTCTGAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT
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                                                                                                                                              exon nucleic acid
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                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                                                                                                 Hanzel
                                                                                                            SEQ
                                                                                                                                                                                                                                                           2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
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                                                                                                                                                                                                                                                 2000GB-0024263
                                                                                                            ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 A; 102 C; 110 G; 125 T; 0 other;
                                                                                                                                                                                                 DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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100.0%;
                                                                                                                                                                                                 Chen
                                                                                                           1510; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            457
                                                                                                                                               probes for analyzing
                                                                                                                                                                                             ž,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 2
                                                                                                                                                                                                  Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               multiple
                                                                                                                                                                                                  DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sclerosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         analysis;
                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 457;
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                                                                                                                                                 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                             s; probe;
schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                format directly
                                                                                                           English
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                                                                                                                                                 in
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183 AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 242

Query Match Best Local Matches

al Similarity 145; Conserv

Conservative

0;

Mismatches

0,

Indels

0;

Gaps

0,

7.18;

Score 145; Pred. No.

2.8e-58;

DB 22;

Length

457;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 145;
                                                                                                                                                                                                                                                    04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 457
                             probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of
Sequence
                                                                          The present invention provides a number of single exon nucleic acid
                                                                                                                   Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow – \,
                                                                                                                                                                                                                                  21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                 09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                     WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK26966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK26966 standard;
                     the probes
                                                                                                Example 4; SEQ ID NO: 1523; 658pp + Sequence Listing; English.
                                                                                                                                                                           Penn SG
                                                                                                                                                                                                (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGAAATAGAGCAACTGCTCTGAT
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                                                                                                                                                     2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                bone
                                                                                                                                                                                                 MOLECULAR DYNAMICS INC
 457
                                                                                                                                                                           Hanzel DK,
                     of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                marrow
                                                                                                                                                                                                                    2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
BP; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 120 A; 102 C;
                                                                                                                                                                                                                                                                                                                                                                                                                               expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08; F1
                                                                                                                                                                                                                                                                                                                                                                                                leukaemia;
A; 102 C; 110 G; 125 T;
                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 457
                                                                                                                                                                                                                                                                                                                                                                                                                               single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             327
                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                                                               lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
2.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                probe
                                                                                                                                                                                                                                                                                                                                                                                                myeloma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 IJ
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                                  treatment of cancers sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                 8
0:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1523
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                                                                                                                                   for
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RESULT 12
AAII1574/c
ID AAII15
XX AAII15
XX Probe;
XW WO2001
XW WO1; 2
XW WWI; 2
XW WWI; 2
XW WWI; 2
XW WWI; 2
XW The processory
CC (SENP)
CC (SENP)
CC Sample
CC Sample
CC Sample
CC Sequen
SQ Sequen
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                                                             Matches
                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                       Sequence 457
                                                                                                                                                              of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cervical cancer;
   450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe #1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI11574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI11574 standard;
                           183 AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-2001
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                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT
AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 391
                                                                                                                                                                                                                                                                                                                                                                                                   2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                 SS
                                                             145;
                                                                                                                                                                                                                                                                                                                                                genome-derived single exon nucleic acid probes useful :
zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                     SEQ ID No 1507; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312
2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-02346359
2000US-0236359
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                                                                                                                       BP; 120 A; 102 C; 110 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                            100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
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                                                                          Score 145;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR
                                                            Mismatches
                                                                         DB 22;
2.8e-58;
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                                                                                        Length
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cervical cell sample
                                                         0;
                                                                                                                                                                                                                                                                                                                                                     s -
                                                         Gaps
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AAI32862/c
ID AAI32862 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04 - FEB - 2000;
26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic actid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-OCT-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-OCT-2001
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                                                 303
                                                                                                                                                                                              450
                                                                                                                                               243
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                                                                                                                                                                                                                                                                                                                 Local
                                                                                         GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT 302
                                                                                                                                                                                                                AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT
TCAGAAATAGAGCAACTGCTCTGAT
                                                 TCAGAAATAGAGCAACTGCTCTGAT
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                                                                                                                                                                                            AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGAAATAGAGCAACTGCTCTGAT 306
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                                                                                                                                                                                                                                                                                   al Similarity
145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID No 1548; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                          Conservative
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2000US-0207456.
2000US-0609408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                      ₿₽;
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                                                                                                                                                                                                                                                                                                                                                                                   120 A; 102 C; 110 G; 125 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Σ
                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                         Score 145; DB 22;
Pred. No. 2.8e-58;
                                                 327
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                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes useful
                                                                                                                                                                                                                                                                                                                                  Length 457;
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RESULT 14

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ABA47966/c
ID ABA47966 standard; DNA; 138
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                                                                                                                                                                                                           The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived CC from human breast and BT 474 cells. The method involves contacting CC the probes with a collection of detectably labelled nucleic acids CC derived from mRNA of human breast, and then measuring the label CC bound to each probe of the microarray. The probes are useful for genemic DNA predicted to cerifying the expression of regions of genomic DNA predicted to CC encode proteins. They are useful for gene discovery, and for CC expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater CC diversity of probes for measuring gene expression, with far less bias CC than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. CC Note: The sequence data for this pattent did not form part of the CC printed specification, but was obtained in electronic format directly CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                Query Match
Best Local
                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-069408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GS-0236559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human breast cell single exon nucleic acid probe #6661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 6661; 327pp + sequence listing;
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                 138
                                                                                 185
                 245
                                               GTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGC 24-
CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC 304
                                                                                                                  al Similarity
138; Conserv
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                                                                                                                  Conservative
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                                                                                                                                                                               Α,
                                                                                                                              6.8%;
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                                                                                                                                                                                 31 C;
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                                                                                                                              Score 138; I
Pred. No. 5.
                                                                                                                                                                                 35 G; 40 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
                                                                                                                  Mismatches
                                                                                                                                                                                   0 other;
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Matches 138;
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26-MAY-2000; 2000US-0208408.
30-JUN-2000; 2000US-0632366.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 14159; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                     Sequence 138
                                                                                                                                                                                                            printed specification, but was obtained in electronic
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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-MODEL-frame+_n2p.model -DEV-x1h
-O-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141247_27244/app_query.fasta_1.2183
-O-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141247_27244/app_query.fasta_1.2183
-O-/cgn2_1/USPTO_spool/US09513151/runat_1504200-1.12p.rai -MINMATCH-0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -STARR-1 -END=-1 -MATRIX=0.13p. -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN=1 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09513151_@cGN_1_1_16_@runat_15042003_141247_27244 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MMAP -LARCEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 17, Appl Sequence 5465, Appl Sequence 5465, Appl Sequence 13, Appl Sequence 13, Appl Sequence 14, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 6, A
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w	e 2, Appl	e 2, Appl	2, Appl	e 2, Aç	2, Ap	e 166,	e 16	4614,	e 11,	10, Ap	nce 4, Appl	o. 54281	e 18,	equence 18, Ap	equence 17,	equence 17,	equence 29, Ap	e 29,	e 8, App	e 8, App	e 8, App	e 8, App	e 8, App	e6,Ap	e 5563,	e 348,	e 325,	equence 287,	e 13, A	e 7, Appl	equence 3, Appl	Sequence 12, Appl

ALIGNMENTS

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RESULT 1
US-09-215-252-17
; Sequence 17, Applic,
; Patent No. 6300487
; Patent No. 6300487
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В
                                                                         US-09-513-151-3 (1-2041) x US-09-215-252-17 (1-378)
                                                                                                                                              Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LEUNG, David W.
APPLICANT: ADOUREL, Daniel
APPLICANT: HOLLENBACK, David
TITLE OF INVENTION: MAMMALIAN LYSOPHOSPHATIDIC
FILE REFERENCE: 077319/0151
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/215,252
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US 08/618,651
PRIOR FILING DATE: 1996-03-19
NUMBER OF SEO ID NOS: 42
                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                 LENGTH: 378
TYPE: PRT
334 SerSerLeuThrLeuAlaSerPhe 341
                                  669 AGTTCTCTAACCCTTGCATCCTTT 692
                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.0
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US-09-513-151-3 (1-2041) x US-09-509-902A-11 (1-505)
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Best Local Similarity:
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US-08-264-002-5
               RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5465, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5465
LENGTH: 666
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 SerValAlaAlaArgAlaVal 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 TCCGTGGCGGCTGCACGAGCAGTT 40
                                                45 LeuGlyAlaThrGlyThrGlyLys 52
                                                                                    95 CTCGGGGCCACGGCACCGGCAAA 118
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Bird, Timothy A.
Anderson, Dirk M.
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100.00%
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Matches:
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Best Local Similarity:
                                                                                                                                                                                                       US-08-999-774A-13
                                                                                                                                                                                                                                                                                                                                                                             Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: P035
TELECOMMUNICATION INCORNATION:
TELEPHONE: 619/455-5100
TELEFAX: 619/455-5110
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                  Sequence 13, Application US/08999774A Patent No. 6274312
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APPLICANT: GUI, JIAN-FANG
APPLICANT: FU, XIANG-DONG
                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: SPENSLEY HORN JUBAS & LUBITZ
STREET: 1880 Century Park East, Fifth Floor
                                                                                                                                                                                                                                                         TITLE OF INVENTION: Intracellular Regulatory Molecules: TITLE OF INVENTION: Related Reagents NUMBER OF SEQUENCES: 13
                                                                              APPLICANT: Gish, Kurt C.
APPLICANT: Seghezzi, Wol
APPLICANT: Shanahan, Fra
APPLICANT: Lees, Emma M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS
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CLONE: CEHK
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NAME: TUMARKIN PH.D., LI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
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CITY: Los Angeles
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                                                                McClanahan, Terrill K.
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Shanahan, Frances
Lees, Emma M.
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DNAX Research Institute

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US-09-513-151-3 (1-2041) x US-08-999-774A-13 (1-1306)
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Best Local Similarity:
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Patent No. 5856127
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US*60/032,818
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO.:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: POWELL, WILLIAM A APPLICANT: MAYNARD, CHARLES !
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 SerAlaLeuGlyIleProSerLeu 644
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STRANDEDNESS: no
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                                   APPLICATION NUMBER: US/08/686,594 FILING DATE:
                                                                                                                                                                                                                        ADDRESSEE: NIXON, HARGRAVE, DEVANS & I
STREET: P.O. BOX 1051, CLINTON SQUARE
CITY: ROCHESTER
STATE: NEW YORK
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                   CLASSIFICATION: 435
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California
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10-DEC-1997
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        Alignment Scores:
Pred. No.:
                                                   ; MOLECULE TYPE: US-08-686-594-4
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Patent No. 5856127
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                 TELEFAX: 716-263-1500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: POWELL, W: APPLICANT: MAYNARD, CTITLE OF INVENTION: AND ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: 716-263-1636
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                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34, J.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TOPOLOGY: li
                                                                                          LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: not rele
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OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 9
US-08-686-594-5
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-08-686-594-1
               Sequence 5, Application US/08686594
Patent No. 5856127
GENERAL INFORMATION:
APPLICANT: POWELL, WILLIAM A.
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2088
TELECOMMUNICATION INFORMATION:
TELECHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 1:
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Patent No. 5856127
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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No.:
APPLICANT: POWELL, WILLIAM A. APPLICANT: MAYNARD, CHARLES A.
                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MAYNARD, CHARLES A.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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STREET: P.O. BOX 1051, CLINTON SQUARE
CITY: ROCHESTER
STATE: NEW YORK
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                                                                                                                                                                                                                                                                                      Matches:
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RESULT 10
US-08-686-594-11
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Best Local Similarity:
Query Match:
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Patent No. 5856127
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                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 2088
TELECOMMUNICATION INFORMATION:
TELECHHONE: 716-263-1636
                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                      APPLICANT: POWELL, WILLIAM A.
APPLICANT: MAYWARD, CHARLES A.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                               CITY: ROCHESTER STATE: NEW YORK
CLASSIFICATION: 435
                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
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                                                                                                                                                              USA
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Query Match:
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US-08-686-594-2
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                                                                                            ; MOLECULE TYPE: US-08-686-594-2
                            Alignment Scores:
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INFORMATION FOR SEQ ID NO: 11:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: MAYNARD, CHARLES A.
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: no
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CITY: ROCHESTER
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                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: no
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                                                                                                                                                                  TOPOLOGY:
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O. BOX 1051, CLINTON SQUARE
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Indels:
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                                                                                                                            US-08-686-594-12
                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                       US-09-513-151-3 (1-2041) x US-08-686-594-6 (1-19)
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Best Local Similarity:
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GENERAL INFORMATION:
                Sequence 12, Application US/08686594
Patent No. 5856127
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 715-20 ID NO: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE HIS SEQUENCE SEQUE
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STREET: P.C.
STREET: NOCHESTER
CITY: NEW YORK
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NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: POWELL, WILLIAM A.
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                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: not TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Matches:
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US-09-513-151-3 (1-2041) x US-08-686-594-12 (1-19)
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Best Local Similarity:
Query Match:
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; MOLECULE TYPE:
US-08-686-594-12
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APPLICANT: POWELL, WILLIAM A.
APPLICANT: MAYNABD, CHARLES A.
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                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: DESCRIPTION DESCRIP
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NUMBER OF SEQUENCES:
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LENGTH: 19 amino acids
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NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/50
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: **
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FILING DATE:
                               APPLICATION NUMBER:
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TYPE: amino acid
STRANDEDNESS: not rele
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CLASSIFICATION: 435
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P.O. BOX 1051,
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ANTIMICROBIAL PEPTIDES
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CLINTON SQUARE
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Matches:
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Indels:
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Alignment Scores:
                             ; MOLECULE TYPE: US-08-686-594-7
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US-08-686-594-7
                                                                                    TELEFAX: 716-203 .... 7:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FRIGTH: 20 amino acids
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Best Local Similarity:
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Patent No. 5856127
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                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,594
FILING DATE:
CIRCUTTON NUMBER: US/08/686,594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOCY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                            REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                         TOPOLOGY:
                                                                    TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: ROCHESTER
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STREET: P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
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                                                                      not relevant
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Pred. No.: 319
Score: 7,00
Percent Similarity: 100.00% Conservative: 100.00% Matches: 000 Matches: 100.00% Conservative: 100.00% Mismatches: 000 Mismatches: 100.00% Mismatches: 100.0

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Command line parameters:

MODEL-frame-_n2p.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26358/app_query.fasta_1.2446
-O=/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26358/app_query.fasta_1.2446
-DB=A_Geneseq_101002 -OFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALICN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=S00 -MINLEN=0 -MAXDL=000000000
-USER=US09513151 @CGN 1_1_84 @runat_15042003_141143_26358 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOPT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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SUMMARIES

No.	Score	Query Match	Length	DВ	ID	Description
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ALIGNMENTS

27-JUN-2002 ABB97295 standard; Protein; АВВ97295; (first entry) AA

Novel human protein

SEQ ID NO:

563.

Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t neuroprotective; antiparkinsonian; protein therapy; EST; expressed sequence tag. gene therapy;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoissis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
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N-PSDB; ABN32481.
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                                                                                                                                            ACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAG
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                      ATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGA
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      ABB10476 standard; Protein; 222
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2000US - 241787P. 2000US - 241808P. 2000US - 241809P. 2000US - 241826P. 2000US - 244617P. 2000US - 246474P. 2000US - 246475P.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders
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       Barnes T,
                                                                                04-MAR-1999
                                                                                                                                     hap-1 gene; cancer; physiological clock.
                                                                                                                                                        gro-1 operon;
                                                                                                                    Caenorhabditis
                         (UYMC-) UNIV MCGILL
                                           25-AUG-1997;
                                                                                                  WO9910482-A1
                                                                                                                                                                           Amino acid sequence of the GRO-1 protein
                                                                                                                                                                                              15-JUL-1999
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                                                                                                                                                                                                                                   AAY02526 standard;
                                                             20-AUG-1998;
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LysProGlnGlu***GlyThrGluLysValIleAspArgLysValGluLeuGluLysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATC
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                                                                                                                                                                                                                                                                      SerHisSerGluPheLeuHisArgGlnHisThrGlyArgLySTrpTrpSerPro
                                                                                                                                                                                                                                                                                         TCTCATAGTGAATTTCTCCATCGTCAACATAC-GGAAGAAGGTGGTGGTCCCCT 654
                                                                                                                                                                                                                                                                                                                              CATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAAACAGGAATC
                                                                                                                                                                                                                                                                                                                                              AspGlyLeuValLeuHisLysArgLeuSerGlnValAspProGluMetAlaAlaLysLeu
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       Hekimi S,
                                                                                                                                                                                             (first
                                                                                                                                                        gro-1 gene;
                                                                                                                   elegans
                                                             98WO-CA00803
                                                                                                                                                                                                                                   Protein;
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       Lakowski B,
                                                                                                                                                      gop-1 gene;
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        Lemieux
                                                                                                                                               gop-2 gene; gop-2
tumour formation;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence rrepresents the GRO-1 protein. The specification describes the five genes of the Caenorhabditis elegans gro-1 operon (AAX36071). The operon contains the gro-1 gene (AAX36072), the gop-1 gene (AAX36072). The gop-2 gene (AAX36075), the gop-2 gene (AAX36075), and the hap-1 gene (AAX36077). The gro-1 gene can be used in a method for the diagnosis and/or prognosis of cancer in a patient. Transgenic mice containing a gene knock-out of a murine gene homologue of the gro-1 gene are useful as models of aging and cancer. The proteins encoded by the genes are useful for identifying compounds that affect the enzymmatic activity of these proteins, in order to enhance longevity of a host and inhibit tumour formation. The gro-1 gene, together with the gop-1, gop-2, gop-3 and hap-1 genes enables stated of a physiological clock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular identity of the gro-1 gene - useful for cancer diagnosis and/or prognosis, and where compounds affecting encoded proteins are useful for enhancing longevity of a host and inhibiting tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-190615/16.
N-PSDB; AAX36072.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           study of a physiological clock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 47-48; 93pp; English.
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                                                                                                                                                                                                                                                             CACATGATCAGCTTTGTGGATCCTCTT---GTGACCAATTACACAGTGGTGGACTTCAGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCAC
                                 AlaLeuLeuLeuHisProAsnAsnArgTyrArgValGlnArgAlaLeuGlnIlePheArg 195
                                                                                                                                                GAGGATGGTCTT-----GTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATG
                                                                                                                                                                                     ThrSerAspAspValAspSerLysSerArgThrSerSerGluSerSerSerGluAspThr 155
                                                                                                                                                                                                                                                                                                    GGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAA-----GTTCTTGTCAAT
                                                                                                                                                                                                                                                                                                                                       GluValThrLeuAspLeuIleLysLysIleArgAlaArgSerLysIleProValIleVal
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                                                                                                           GluGluGlyIleSerAsnGlnGluLeuTrpAspGluLeuLysLysIleAspGluLysSer 175
                                                                                                                                                                                                                                                                                                                                                                           AATAGAGCAACTGCTCTGATTGAAGATATTTTGCCCCGAGACAAAATTCCTATTGTTGTG
                                                                        GCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAA 589
                                                                                                                                                                                                                          ACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAG
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hap-1 gene; cancer; aging; longevity;
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                                                                                                                                                                                                                                                                    The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and ofher genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and proteins encoded by it are useful in pharmaceutical and proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful in pharmaceutical and the proteins encoded by it are useful the proteins encoded by it are useful the pharmaceutical and the proteins encoded by it are useful to the proteins are proteins encoded by it are proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides \dot{\,}
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                                                                         Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly fro at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                            monocytogenes and related organisms.
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Alignment Scores: Pred. No.:

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|GlyIleGlyTyrLysGluLeuPheProTyrPhe-----
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                                                                                                               ACTAGTAACCAGCTTCTAAAGAAA
                                                                                                                                                                        TCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAG
                                                                                                                                                                                                      LeuTyrAspGlnHisLeuValAspValProAla---
                                                                                                                                                                                                                                 CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA
                                                                                                                                                                                                                                                            GlnArgValAsnLeuMetPheGluGluGlyLeuValThrGluAlaLys-----Lys
                                                                                                                                                                                                                                                                                         AAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTTGGAGGAACTAAGAGATTTTCACAGA 793
                                                                                                                                                                                                                                                                                                                    TyrLysProLeuPheLeuGlyLeuAspLeuAspArgAlaLeuLeuTyrGluArgIleAsn
                                                                                                                                                                                                                                                                                                                                                TCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGCTTGGAT
                                                                                                                                                                                                                                                                                                                                                                              GlnValHisAsnValLeuAsnAspThr ........
                                                                                                                                                                                                                                                                                                                                                                                                         ---CTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAGGCCAGCGGCTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACC 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCA 316
                           Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CC (II), given in AAGS1454 to AAGS3120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used (I) and (II) can have antibacterial activity and therefore can be used (I) and (II) can have antibacterial activity and therefore can be used (I) vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the curvaturent of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing off the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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N-PSDB; AAH53033.
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                                                                                                                                                   CTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGC
                 ATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGC
                                                       LysLysPheAsnGlyGluIleIleSerGlyAspSerMetGlnValTyrGlnGlyMetAsp
                                                                                          CAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGAC
                                                                                                                                 LeuIleValIleValGlyProThrAlaSerGlyLysThrGluLeuSerIleGluValAla
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Indels:
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Conservative:
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                             Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-2002 (first entry)
(FARB ) BAYER AG
                                                   28-AUG-2001; 2001WO-EP09892
                                                                                                        28-AUG-2001;
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                                                   CGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCT
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                                                                        Essential bacterial genes from Haemophilus influenzae and methods for identifying 'essential' genes that may be potential therapeutic targets
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Page 75-76; 185pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF94345 to AAF94409 represent essential bacterial genes from Haemophilus influenzae, which encode the proteins given in AAB88492 to AAB88556. The present invention also describes methods for identifying essential bacterial genes (i.e. those essential to the survival of a bacterium) using a transposition system. The methods are used to identify essential genes from bacteria, especially H. influenzae (which causes ottits media, meningitis and upper respiratory tract infections) which may be used as targets for potential antimicrobial agents.

AAF94410 to AAF94416 represent PCR primers used in the exemplification
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                                 GlnArgPheHisLysMetIleGluLeuGlyPheGlnAlaGluValGluLysLeuTyrAla
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                                                                                                                                                                                                                                                                                                                       LeuHisThrGluLeuAlaLysIleAspProIleSerAlaAlaArgIleAsnProSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGTGATTGACCGAAAAGTGGAGCTTGAA------AAGGAGGATGGTCTTGTA 493
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Best Local Similarity:
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                                                                                                                                                   The invention describes an essential bacterial gene (I) comprising a purified polynucleotide isolated from Haemophilus influenzae where (I) is essential to H. influenzae survival. The encoded polypeptide (II) is useful for screening substances that function to inhibit essential H. Influenzae polypeptides by contacting (II) with the desired substances and measuring the response by a screen from specific, enzyme, general, affinity, phenotypic and binding screen. (I) and (II) are useful in developing therapeutic agents such as antifungal, antibacterial and developing therapeutic agents such as antifungal, antibacterial and antiparasitic agent, insecticidal agent, and preventive antimicrobial agents which are effective in preventing microbial infection or useful in treatment of that particular infection. (I) and (II) may also be useful in treatment of mucous membrane infections such as otitis media, sinusitis, bronchitis, alveolitis, conjunctivitis, pneumonia, meningitis, epiglottis, cellulitis and septic arthritis. This is the amino acid
                                                                                                                                        epiglottis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Essential bacterial genes in Haemophilus influenzae necessary for bacterium's growth and survival, useful for screening inhibitors polypeptides and developing therapeutic agents e.g. antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Essential bacterial gene; antifungal agent; antibacterial agent; antiparasitic agent; insecticidal agent; microbial infection; mucous membrane infection, otitis media; sinusitis; bronchitis; alveolitis; conjunctivitis; pneumonia; meningitis; epiglottis;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 75-76; 185pp; English.
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	fragment SEQ II l transduction mapping; gene (
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                                    ATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGC::::::::||||||||||||::::::
TTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCT 322
                        ValLeuThrAsnLysValThrProLysGluCysArgGlyValProHisHisLeuLeuGly
                                                               ThrargPheGlnGlyGluIleIleAsnSerAspLysIleGlnLeuTyrLysGlyLeuAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 1616; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                             383 TACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACT 442
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TyrIleGluAlaLeu---
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                                                           AlaIleSerLysLeuSerAlaAsnAsnLysLeuProIleValAlaGlyGlySerAsnSer 135
                                                                                         ValPheAspSerGluAlaGlyAsnLeuThrAlaThrGlnTyrSerArgLeuAlaSerGln 115
                                                                                                                                                        TTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCT 322
                                                                                                                                                                                      ValLeuThrAsnLysValThrProLysGluCysArgGlyValProHisHisLeuLeuGly 95
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FR2807446-A1.	FX	
actococcus	La	
Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.	B 1	
Lactococcus lactis protein miaA.	Lac	
16-MAY-2002 (first entry)	16-	
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JLT 14 33936 ABB53936 standard; Protein; 294 AA.	> 0 H	
laAlaSerTyrGlyGlyGlySerGlySerArgAlaHisA	Db 31	
ATCGAATCATCATTGGGGATCGCGAA	-	
302AsnGlnLeuLysAsnAspAspValGluHis-Cys 312	Db 30	
AAGCTGAGAACAAGAGAAGTTAT	0	
alAlaArgProSerGluArgIleValAspLysPh	Db 28	
TGAACCTGCTTGAAATCGTGCAAAGTTTCATCCAGGGCCA	0	
266 AlaThrGluValPheLeuLysArgAsnValGluGluGlnAspGluAlaTrpGluAsnLeu 285	Db 26	
CTGATGTCTCGAAGTGGG	ОУ 97	
246 GlnLeuLysLysIleGlnArgLeuHisLysLysTrpLysMetSerMetHisArgValAsp 265	Db 24	
CTATGGCTTAGA	Оу 95	
226 LysMetLeuAspValAlaValLysAsnIleLysLysAsnThrGluIleLeuAlaCysArg 245	Db 23	
GCTTCTAAAGAAAGGACCTG		
206 ValProGluLeuHisGluTyrLeuArgAsnGluSerLeuValAspArgAlaThrLysSer 225	Db 20	
AAAATGCACACTGGAGACTAGTAA		
192 ProLysAlaAsnTyrSerValGlyIleArgArgAlaIleGly 205		
ACATGGTATCTTCCAATCAATTGG		
\laGlyLeuLeuGluGluValArgGluVal-	Db 17	
ACATGCTTGCTGCGCCTCTTGGAGGAACTAAGAGATTTTTCACAGACGC	Qy 74	
PheIleTrpValAspValSerLeuProValLeuAsnSerPheValSerLysArgVa	Db 15	
GCATCCTTTGGCTTCATGCTGACCAGG		
lyPheLeuLeuAsnAsnTyrAs	Db 14	
623 CGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCT 682		
141 145	Db 14	
563 GTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTTCTCCAT 622	0у 5	
140 140	Db 14	
503 CGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATGACAAACGCAAA 562		
140 140	Db 1	
443 GAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAA 502	Qy 4.	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                               GlnGluAsnHisGluGluMetMetLysLeuArgGluGluLeuSerLeuLeuSerAspGlu
                                                                                          GAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTA-----
                                                                                                                      TyrileGinSerLeuile
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|LeuIleLysGluIleLeuAspGlnGlyLysValProIleIleValGlyGlyThrGlyLeu
                                                                                                                                                                                                       CTGATTGAAGATATTTGCCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTAT
                                                                                                                                                                                                                                ---ValArgLysTrpThrGluAsnPheSerValHisAspPheValIleGluAlaAsnGln
                                                                                                                                                                                                                                                            TTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCT
                                                                                                                                                                                                                                                                                      ATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGC
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                                     -CTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACAT
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99US-0127462.

99US-0128334.

99US-0128714.

99US-0129845.

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99US-0130891.

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-AUG-1999 99USAUG-1999 99USSEP-1999 99USSEP-1999 99USSEP-1999 99USSEP-1999 99USSEP-1999 99USSEP-1999 99USSEP-1999 99US-	-JUL-1999; 99US-C-JUL-1999; 99US-C-JUL-1
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33 4 80	CTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGAT	275 61	8
274 60	AAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCT ::: ::: ::::::		β δ
214 40	GGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAAC	155 21	B &
154 20	TCGGGGCCACGGCACCGGCAATCCACGCTGGCGTTGCAGCTAGGC:: :::		Оy
	-151-3 (1-2041) x AAG49766 (1-290)	-09-513	SD
	Scores: 4.38e-26 Length: 290 327.50 Matches: 99 imilarity: 38.58% Conservative: 53 il Similarity: 25.13% Mismatches: 104 9.16% Indels: 138 ch: 916% Gaps: 9	ignment ed. No. ore: rcent S st Loca ery Mat	Al Pr Sc Pe Be DB
	-OCT-1999; 99US-0160989OCT-1999; 99US-0161404OCT-1999; 99US-0161405OCT-1999; 99US-0161405OCT-1999; 99US-0161350OCT-1999; 99US-0161361OCT-1999; 99US-0161361OCT-1999; 99US-0161361OCT-1999; 99US-0161931OCT-1999; 99US-0161993OCT-1999; 99US-0161993OCT-1999; 99US-0161993.	22 22 25 25 26 26 26 26 26	PR P

Qy 1139 ATCATCA: ::: Db 275 aAlaSer'	Db 263	Qy 1079 ATGCCA	Db 251 SerGlu	Qy 1019 GCTCTT	Db 231 PheLeu	Оу 989	Db 211 IleGln	Qу 956	Db 191 ValAla	Qy 932	Db 171 HisGlu	. Qy 875 CACGAG
.139 ATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAAT 1178 ::: ::: 275 aAlaSerTyrGlyGlySerGlySerArgAlaHisAsn 288	o o	1079 ATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGTGATCGA 1138	SerGluArgIleValAspLysPheTyrAsnAsnAsn	GCTCTTGAAATCGTGCAAAGTTTCCATCCAGGGCCACAAGCCTACAGCCCACTCCAATAAAG 1078	PheLeuLysArgAsnValGluGluGlnAspGluAlaTrpGluAsnLeuValAlaArgPro 250	AGTCI	211 IleGlnArgLeuHisLysLysTrpLysMetSerMetHisArgValAspAlaThrGluVal 230	TATGCTTATGGCTTAGAGGTATCTGATGTC	191 ValAlaValLysAsnTleLysLysAsnThrGluIleLeuAlaCysArgGlnLeuLysLys 210	AAGAAAGGACCTGGTCCCATTGTC	HisGluTyrLeuArgAsnGluSerLeuValAspArgAlaThrLysSerLysMetLeuAsp 190	CACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAGACTAGTAACCAGCTTCTA 931
	275	1138	262	1078	250	1018	230	886	210	955	190	931

Search completed: April 21, 2003, 18:48:16 ...Job time: 80.8325 secs

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-Q-/cgn2_1/USFTO_spool/US09513151/runat_15042003_141248_27291/app_query.fasta_1.2183
-DB-Pending_Patents_AA_New -QFMT=fastan -SUFETX-olinzp_rapn -MINNATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-oligo
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1
-ALIGN=15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09513151_@CGN_1_1_49_@runat_15042003_141248_27291
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELEXT-7
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9162.495 Million cell updates/sec
563, App
7968, Ap
7967, Ap
7967, Ap
7969, Ap
7969, Ap
11847, Ap
81141, Ap
16934, A
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Query Match:
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US-10-380-731-563
                                                                                                                       US-09-513-151-3 (1-2041) x US-10-380-731-563 (1-411)
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US-10-380-731-563
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PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 888
SOFTWARE: Custom
SEQ ID NO 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 563, Application US/10380731 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HYSEG, INC
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-114
CURRENT APPLICATION NUMBER: US/10/380,731
CURRENT FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                                                                                   LENGTH: 411
TYPE: PRT
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US-10-282-122A-46768
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US-10-366-683-18438
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US-09-134-000C-4333

US-09-134-000C-4333

US-10-366-683-30556

PCT-US02-36123-2920

PCT-US02-32727-25977

US-10-057-498-25-977

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US-10-057-498-26977
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US-10-282-122A-48736
US-09-864-408A-124
US-10-366-683-18739
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US-10-366-683-17702
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Conservative:
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Command line parameters:
-MODEL-frame+_n2p.model -DEV-xlh

Post-processing: Listing first 45 summaries

Database :

Pending_Patents_AA_New:*

7654321

/cgn2_6/ptcdata/2/paa/PCT_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptcdata/2/paa/US10_NEW_COMB.pep:*
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Result

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SUMMARIES

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US-10-380-731-563 US-60-453-135-7968 US-60-453-135-7967 US-60-453-135-7967 US-60-453-050-7969 US-60-453-050-7969 US-60-453-050-7969 US-60-453-050-7969 US-10-203-138A-11847 US-10-366-683-25445 US-10-366-683-16934

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seq length: 0 seq length: 2000000000

Total number of hits satisfying chosen

parameters:

1386358

Searched:

714767 seqs, 157122656 residues

Sequence:

Perfect score:

US-09-513-151-3 661 1 CTGCCATAAGATGG

CTGCCATAAGATGGCGTCCG.

Scoring table:

Xgapop Ygapop Fgapop OLIGO

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nucleic on:

protein search, using frame_plus_n2p model

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compus

Compugen Ltd

April 21, 2003, 19:14:35; Search time 70 Seconds

US-09-513-151-3

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Sequence 7968, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7968
US-60-453-135-7968
US-60-453-135-7968
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 7968
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
                                                                                                                                                                                     TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US FILE REPERENCE: CL001457
                                                                                                            LENGTH: 475
TYPE: PRT
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Alignment Pred. No.:

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Query Match:
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Best Local Similarity:
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                                                                      APPLICANT: CARGILL, Michele
APPLICANT: INKOUBOVA, Olga
APPLICANT: INKOUBOVA, Olga
APPLICANT: INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION
TILE REFERENCE: CLOO1456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SED ID NOS: 82762
SOFTWARE: FASUSED for Windows Version 4.0
SEQ ID NO 7967
LENGTH: 221
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US-60-453-050-7967
                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele
APPLICANT: LUKE, MAY
APPLICANT: LUKE, MAY
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001457
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7967
LENGTH: 221
                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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TYPE: PRT
ORGANISM:
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Matches:
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Alignment Scores:
Pred. No.:
                                                                                                       ; ORGANISM: Homo US-60-453-050-7969
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                                                                                                                                                      NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEO for Windows Version 4.0
SEQ ID NO 7969
LENGTH: 85
                                                                                                                                                                                                                                                                                    Sequence 7969, Application US/60453050 GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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; TYPE: PRT
; ORCANISM: Homo sapiens
US-60-453-135-7969
                                                                                                                                                                                                                                TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/60/453,050 CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US_60-453-135-7969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7969, Application US/60453135
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER, US/60/453,135
CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DEFILE REFERENCE: CL001456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1199
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                                                                                                                      sapiens
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                                 63
85
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PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 21 September 2000 (27.09.00)

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)

NUMBER OF SEQ ID NOS: 15438

SEQ ID NO 11847

LENCTH: 57

TYPE: PRT
           Best Local Similarity:
Query Match:
                                          Percent Similarity:
                                                                                       Alignment Scores:
                                                                                                                    ; OTHER INFORMATION: US-10-203-138A-11847
                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/236, 312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR FILING DATE: 03 August 2000 (30.08.00)
PRIOR APPLICATION NUMBER: US 09/632, 366
PRIOR APPLICATION NUMBER: US 60/236.3
PRIOR APPLICATION NUMBER: US 60/236.3
PRIOR APPLICATION NUMBER: US 60/236.359
PRIOR APPLICATION NUMBER: US 60/236, 359
PRIOR FILING DATE: 27 September 2000 (27.09.00)
PRIOR FILING DATE: 27 September 2000 (27.09.00)
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US-10-203-138A-11847
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DB:
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OTHER INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11847, Application US/10203138A
                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AL033527.25
                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 WO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Molecular Dynamics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1199 CTGAAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTT 1258
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Rank, David R.
Hanzel, David K.
Chen, Wensheng
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                              Length:
Matches:
Conservative:
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US-10-366-683-25445

APPLICANT: Deloughery, Craig APPLICANT: Bush, David APPLICANT: Rubenfield, Marc J. APPLICANT: Nolling, Jork Ş В Ş

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US-09-513-151-3 (1-2041) x US-10-366-683-25445 (1-254)
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US-10-366-683-25445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25445, Application US/10366683 GENERAL INFORMATION:
                                                                                                        TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATH03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 GTTGCAGCTAGGCCAGCGGCTCGGCGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACACTGGTGGACCTTC 30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAsnArgAlaThrAlaLeuIle 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10369493
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APPLICANT: ISHKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SKAKKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CCURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13800
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US-10-156-761-13800
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Best Local Similarity:
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PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16934
LENGTH: 387
TYPE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-513-151-3 (1-2041) x US-10-369-493-8141 (1-365)
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Best Local Similarity:
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APPLICANT: Rubenfield, Marc J.
APPLICANT: Nolling, Jork
APPLICANT: Nolling, Jork
APPLICANT: Deloughery, Craig
APPLICANT: Description: Craig
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOM
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                        APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PATH03-04
CURRENT APPLICATION NUMBER: US/10/366,683
CURRENT FILING DATE: 2003-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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В Ş Best Local Similarity:

100.00% 100.00% 1.36% 8.05 9.00

Percent Similarity:

Pred. No.: Alignment Scores:

NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 25445 LENGTH: 254

TYPE: PRT

Query Match:

US-10-369-493-8141

Sequence 8141,

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng

NUMBER OF SEQ ID NOS: 47374 SEQ ID NO 8141 LENGTH: 365

ORGANISM: Thermobifida fusca

TYPE: PRT

LENGTH: 713

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Best Local Similarity:
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                                                                    Alignment Scores:
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Percent Similarity:
Best Local Similarity:
                                                 Pred. No.:
                                                                                                        US-10-282-122A-48736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 48736
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CURRENT APPLICATION NUMBER: US/10/282,122A •
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                             Remaining Prior Application data removed . NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/230,347 PRIOR FILING DATE: 2000-09-09
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                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/2 PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                       ORGANISM: Bacteroides fragilis
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                                                                                                                                                            LENGTH: 124
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Zyskind, Judith
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Query Match:
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                                                     Percent Similarity:
                                                                                           Pred. No.:
                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa US-10-366-683-18739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-366-683-18739
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                                                                                                          Alignment Scores:
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APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets Novel Human Polynucleotides and Polypeptides Encoded There.
TITLE OF INVENTION: Novel Human Polynucleotides and Polypeptides Encoded There.
TILE REFERENCE: 21402-012
CURRENT APPLICATION NUMBER: US/09/864,408A
CURRENT FILING DATE: 2001-05-24
CURRENT FILING DATE: 2001-05-24
                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/252,991
PRIOR FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18739
LENGTH: 200
TYPE: PRT
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PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 124
LENGTH: 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18739, Application US/10366683
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                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/366,683 CURRENT FILING DATE: 2003-02-13
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: PATH03-04
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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Bush, David
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Ygapop 60.0 , Ygapext
Fgapop 6.0 , Fgapext
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
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	Sequence 153, App Sequence 151, App Sequence 151, App Sequence 151, App Sequence 184, App Sequence 784, App Sequence 789, App Sequence 789, App Sequence 7892, App Sequence 7894, App Sequence 7894, App Sequence 5741, App Sequence 5804, App Sequence 10491, App Sequence 11815, App Sequence 11815, App Sequence 11815, App Sequence 11834, App Sequence 11835, App Sequence 11834, App Sequen	Description

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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo
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TYPE: PRT
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FILING DATE: 2001-08-10
APPLICATION NUMBER: 60/325,102
FILING DATE: 2001-09-26
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APPLICATION NUMBER: 60/324,967
FILING DATE: 2001/09/26
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TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/314,967

PRIOR APPLICATION NUMBER: 60/314,967

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-16

PRIOR FILING DATE: 2001-09-19

NUMBER OF SECONDO 10 NOSE: 363-180

PRIOR FILING DATE: 2001-09-19
               Percent Similarity:
Best Local Similari
Query Match:
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US-10-097-340-153
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Rachel E. MEYERS
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PCT-US02-07826-151
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For
TITLE OF INVENTION: Assessment, Prevention, and Therapy of
                                        Sequence 151, Application
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Query Match:
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PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/25,149
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/224,967
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
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CURRENT APPLICATION NUMBER: PCT/US02/07826
CURRENT FILING DATE: 2002-03-14
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CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/325,149
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PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
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PRIOR APPLICATION NUMBER: 60/276,026
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                           Percent Similarity:
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                   Query Match:
                                                                       Alignment Scores:
Pred. No.:
                                                                                                             ; ORGANISM: Homo sapiens
US-10-097-340-151
                                                                                                                                               PRIOR APPLICATION NUMBER: 60/32
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows V
SEQ ID NO 151
LENGTH: 465
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                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: MRI-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                       TYPE: PRT
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Gordon B. MILLS
Robert C. BAST,
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Rachel E. MEYERS
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Shubhangi KAMATKAR
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PCT-US01-01239-1394

Sequence 1394, Application PC/TUS0101239

GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PT213PCT

CURRENT APPLICATION NUMBER: PCT/US01/01239

CURRENT ETILING DATE: 2001-01-17
Prior application data removed
NUMBER OF SEQ ID NOS: 2318
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1394
LENGTH: 222
TYPE: PRT
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                                                                                                                                                                                                                                                      PCT-US01-01349-586
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION:
PCT-US01-01349-586
                                                                                                                                                Sequence 586, Application PC/TUS0101349
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06PCT
CURRENT APPLICATION NUMBER: PCT/US01/01349
CURRENT FILING DATE: 2001-01-14
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 939
                                                                                                              SEQ ID NO 586
LENGTH: 222
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LOCATION: (145)
OTHER INFORMATION:
                                                                                                                                      SOFTWARE: PatentIn Ver.
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LOCATION: (124)
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                                          NAME/KEY: SITE LOCATION: (124) OTHER INFORMATION:
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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   US-09-513-151-3 (1-2041) x PCT-US01-01349-784 (1-222)
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NAME/KEY: SITE
LOCATION: (124)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (145)
OTHER INFORMATION: X
PCT-USO1 01349-784
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Best Local Similarity:
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PCT-US01-01349-784
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        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                       Sequence 784, Application PC/TUS0101349
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06PCT
CURRENT APPLICATION NUMBER: PCT/US01/01349
CURRENT FILING DATE: 2001-01-14
                                                                                                                                                                                                                         Prior application data removed -
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 784
                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                              FEATURE
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM
NUMBER OF SEQ ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 586
LENGTH: 222
TYPE: PRT
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OTHER INFORMATION: :
NAME/KEY: SITE
LOCATION: (145)
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
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LOCATION: (124)
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GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic
FILE REFERENCE: PJZ06
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SEQ ID NO 784
LENGTH: 222
TYPE: PRT
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LOCATION: (124)
OTHER INFORMATION: 1
NAME/KEY: SITE
LOCATION: (145)
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CURRENT FILING DATE: 2001-01-17
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US-09-764-902-1394
RESULT 11
US-10-072-326-586
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LOCATION: (124)
OTHER INFORMATION: >
NAME/KEY: SITE
LOCATION: (145)
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1394
LENGTH: 222
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TITLE OF INVENTION: Nucleic Acids, Proteir
FILE REFERENCE: PTZ13
CURRENT APPLICATION NUMBER: US/09/764,902
CURRENT FILING DATE: 2001-01-17
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Query Match:
Sequence 784, Application US/10072326
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06C1
CURRENT APPLICATION NUMBER: US/10/072,326
CURRENT FILING DATE: 2002-02-11.
Prior Application removed - See File wrapper
NUMBER OF SEQ ID NOS: 939
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SEQ ID NO 586
LENGTH: 222
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06C1
CURRENT APPLICATION NUMBER: US/10/072,326
CURRENT FILING DATE: 2002-02-11.
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Sequence 2199, Application US/09757028

GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant FILE REFERENCE: PM001
CURRENT APPLICATION NUMBER: US/09/757,028
CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
                          ; TYPE: PRT; ORGANISM: Homo sapiens
US-09-757-028-2199
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Alignment Scores
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                                                                SOFTWARE: PatentIn Ver.
SEQ ID NO 2199
LENGTH: 143
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LENGTH: 222
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LOCATION: (124)
OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/757,028
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                   SEQ ID NO 2199
LENGTH: 143
TYPE: PRT
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM001C1N
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                           1001 GAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCT 1060
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN HUMAN PLACENTA FILE REFERENCE: PB 0004 WO 7

CURRENT APPLICATION NUMBER: PCT/US01/00663

CURRENT FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/180, 312

PRIOR FILING DATE: 03 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 09/532, 366

PRIOR APPLICATION NUMBER: US 09/532, 369

PRIOR APPLICATION NUMBER: US 09/532, 369

PRIOR FILING DATE: 03 October 2000 (03.10.00)

PRIOR APPLICATION NUMBER: US 60/234, 687

PRIOR FILING DATE: 27 September 2000 (27.09.00)

PRIOR FILING DATE: 21 September 2000 (21.09.00)

PRIOR FILING DATE: 31 September 2000 (21.09.00)

PRIOR FILING DATE: 31 September 2000 (30.06.00)

PRIOR FILING DATE: 30 June 2000 (30.06.00)
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SOFTWARE: Molecular Dynamics Sequence Listing Engine SEQ ID NO 27779
LENCTH: 57
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OTHER INFORMATION:
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Hanzel, David K.
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EST_HUMAN HIT: BE242161.1, EVALUE 3.00
SWISSPROT HIT: Q9KAC3, EVALUE 2.00e-04
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-LOOPEXT-0 -UNITS-bits -START-1 -RND--1 -MATRIX--oligo -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09513151_@CGN_1_1_112_@runat_15042003_141246_27221 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGING -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPDP-60 -XGAPDXT-60 -FGAPDXT-7
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         Lemieux J., Lakowski B., Webb A., Meng Y., Ubach A., Bussiere F. Barnes T., Hekimi S.;
"Regulation of Physiological Rates in Caenorhabditis elegans by trNA-Modifying Enzyme in the Mitochondria.";
Genetics 159:147-157(2001).
EMBL; AY052768; AALJ4107.1;
InterPro; IPR002627; IPPT.
InterPro; IPR00822; Znf_C2H2.
Pfam; PF07715; IPPT; 1.
                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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  PD004674;
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TIGRFAMS; TIGR00174; miaA; 1.
PROSITE: PS00028; ZINC_FINGER_C2H2_1;
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MEDLINE=20544178; PubMed=11111046;
GOLOVKO A., Hjalm G., Sitbon F., Nicander B.;
GOLOVKO A., Hjalm G., Sitbon F., Nicander B.;
"Cloning of a human tRNA isopentenyl transferase.
Gene 258:85-93(200).
EMBL; AF074918; AAG31324.1; -.
EMBL; AF074918; AAG31324.1; -.
InterPro; IPR000822; IPPT.
InterPro; IPR000822; Znf_CCH2.
Pfam; PF01715; IPPT; 1.
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HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
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SEQUENCE 4
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TIGRFAMS; TIGR00174; miaA; 1.
proSITE; pS00028; ZINC_FINGER_C2H2_1;
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                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
CDNA FLJ20061 fis, clone COL01383.
                                                                                                                                                                                                                                   Q9NXT7
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                      TISSUE-COLON;
                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                       PRELIMINARY;
     Hikiji
                                                                                            Chordata;
Primates;
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       Kobatake
                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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         Ikema
         Okamoto
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Percent Similarity:
Best Local Similarity:
Query Match:
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Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databa:
EMBL; AKOO0068; BAA90923.1; -.
Interpro; IPR0002627; IPPT.
R Interpro; IPR0002627; IPPT.
R Interpro; IPR000822; Znf_CZH2.
R Pfam; PF01715; IPPT; 1.
R PFODOM; PD004674; IPPT; 1.
R PFODOM; PD004674; IPPT; 1.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; UNKNOWN_1.
SEQUENCE 326 AA; 37435 MW; EAB3F0F9664B7ACE CRC6
                                                                                                                                            Q96FJ3 PRELIMINARY; PRT; 324 AA.
Q96FJ3;
Q96FJ3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to tRNA isopentenylpyrophosphate transferase.
                                                                                Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; [
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SEQUENCE FROM N.A TISSUE=UTERUS;
                                           NCBI_TaxID=9606;
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169.00
100.00%
100.00%
25.57%
                                                                                                           Chordata;
                                                                                       Primates;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                           Vertebrata;
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Best Local Similarity:
Query Match:
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DR
DR
DR
DR
DR
DR
SQ
                                         Q9D1H5 PRELIMINARY; PRT; 326 AA.
Q9D1H5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
2310075G14RIK protein (RIKEN cDNA 2310075G14 gene).
2310075G14RIK....
               Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (JUL-2001) to the EMBI
Submitted AAH10741.1;
InterPro; IPR002627; IPPT
InterPro; IPR000822; Znf_C2H2.
Pfam; PF01715; IPPT; 1.
SEQUENCE FROM N.A.
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SEQUENCE
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SMART; SM00355; ZnF_C2H2;
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                                                                                                                                                                                                                                                                                                                                                                       LeuHisLysArgLeuSerClnValAspProGluMetAlaAlaLysLeuHisProHisAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.13e-117
119.00
96.53%
96.53%
18.00%
                        Rodentia;
                                Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37223 MW;
                     Sciurognathi; Muridae;
                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
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                                                                                                                                                    940
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Matches:
Conservative:
Mismatches:
Indels:
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167
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashina J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashizaki Y.:
                                                                                              01-MAY-2000
01-MAY-2000
01-MAR-2002
Pseudomonas stutzeri (Pse
Bacteria; Proteobacteria;
Pseudomonas.
NCBI_TaxID=316;
[1]
                                                                       PILU.
                                                                                   Putative
                                                                                                                                           Q9RLD5;
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Interpro; IPR002627; IPPT.
Interpro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1
ProDom; PD004674; IPPT; 1
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1
SEQUENCE 326 AA; 37191 MW; 454367A8B70DD1F0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the ENEMBL; AK003556; BAB22853.1; --
EMBL; BC019812; AAH19812.1; --
                                                                                                                                                                                                                                          614
                                                                                                                                                                                                                                                             Strausberg R. Submitted (DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE=21085660; PubMed=11217851;
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                                                                                           ) (TrEMBLrel.
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) (TrEMBLrel.
                                  stutzeri (Pseudomonas perfectomarina)
roteobacteria; gamma subdivision; Pseu
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Lrel. 13,
Lrel. 20,
protein.
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Last sequence up
Last annotation
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Matches:
Conservative:
Mismatches:
Indels:
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DB:
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opportunistic pathogen.";
Nature 406:959-964(7000).
EMBL; 127667; AAA25965.1; -.
EMBL; AE004477; AAG03785.1; -.
Interpro; IPR001482; GSPII_E.
Pfam; PF00437; GSPII_E; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graupner S., Weger N., Sohni M., Wackernagel W.;

"Requirement of bovel competence genes pilT and pilU of Pseudomonas stutzeri for natural transformation and suppression of pilT deficiency by a Hexahistidine tag on the type IV Pilus protein PilAI.";

J. Bacteriol. 183:4694-4701(2001).

EMBL; AJ249385; CAB56296.1;

EMBL; AJ249385; CAB56296.1;

InterPro; IPR001482; GSPII_E.

Pfam; PF00437; GSPII_E: 1.

ProDom; PD000739; GSPII_E: 1.

SEQUENCE 381 AA; 42417 MW; C69B6E6BC24EA3DB CRC64;
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Q51532;
                                                                                                     SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Hickey M.J., Brinkman F.S.L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Barody L.L., Goltry L., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
PILU (Twitching motility protein PILU).
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STRAIN=JM300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
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MEDLINE-91285432; PubMed-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                            "Characterisation of a Pseudomonas aeruginosa twitching motility gene
                                                                                                                                                                                                                                                                                                                                                                                                                      Whitchurch C.B., Hobbs M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=287;
                                                                                         "Complete genome sequence of Pseudomonas aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130
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15692 / PAO1;
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Q9UT75;
Q1-MAY-2000
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Complete proteome.
SEQUENCE 382 AA;
Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; Erspermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                            Murphy L., Harris D., Wood V., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ de EMBL, AL109739; CAB52278.1; - InterPro; IRR002627; IPPT. Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tRNA isopentenyltransferase.
SPAC343.15.
                                                                      Q8S9Z6;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomycetales; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                    Similar to tRNA isopentenyltransferase. OJ1656_A11.14.
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Matches:
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Indels:
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                        Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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RESULT 11
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                                                                US-09-513-151-3 (1-2041) x Q9QY56
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Best Local Similarity:
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InterPro; IPR001092; HLH_basic.

InterPro; IPR000822; Znf_C2H2.

Pfam; PF00096; Zf-C2H2; 10.

SMART; SM00355; ZnF_C2H2; 9.
                                                                                                                                                                         PROSITE; PS5015
DNA-binding; Me
SEQUENCE 783
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Lebedeva T.V., Singh A.K.;

Lebedeva T.V., Singh A.K.;

"Repression of the murine II-1 beta expression by the mu
E4F transcription factor.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF126967; AAF22563.1;

HSSP; P15822; 3ZNF.
                                                                                                                                             No.:
                             387
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                                                                                                    Match:
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Mammalia; Eutheria;
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:OJ1656_A11.",
Submitted (MAR-2001) to the EMBL/GenBa
EMBL; AP003448; BAB85325.1; -.
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SEQUENCE FROM
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                                    GAGGAGTCTGTTCTTGAACCTGCTCTT
                        GluGluSerValLeuGluProAlaLeu 395
                                                                                                                                                                    PS00038; HELIX LOOP_HELIX; UNKNOWN_1.
PS00028; ZINC_FINGER_C2H2_1; 6.
PS50157; ZINC_FINGER_C2H2_2; 9.
ling; Metal-binding; Zinc-finger.
1109; Metal-binding; 2inc-finger.
1109; Metal-binding; 2inc-finger.
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Sciurognathi;
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RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroy(RA) Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M. Whitehead S., Barrell B.G.;

"The genome sequence of the food-borne pathogen Campylobacter Treveals hypervariable sequences.";
Nature 403:665-668 (2000).
          RESULT
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Q9PIX9;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=NCTC 11168; MEDLINE=20150912;
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                 Hypothetical CJ0148C.
                                                                                                                                                                                                                                                                            NCBI_TaxID=197;
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Sampei G., Motomura K., Masuda S., Yamaguchi Furuya N., Komano T., Mizobuchi K.;
"Organization and diversification of plasmid nucleotide sequence of the R721 genome.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence of the R721 shufflon.
J. Bacteriol. 174:7053-7058(1992).
EMBL: AP002527; BAB12655.1;
InterPro; IPR004346; CagE_TrbE_VirB.
Pfam; PF03135; CagE_TrbE_VirB; 1.
Plasmid.
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01-JUN-2002
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MEDLINE-93015772; PubMed-1400257;
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013503;
01-JAN-1998
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01-JUN-2001
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  Pleurotus
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Ifuku Y.,
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RESULT
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                                                                                                                                                 radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001919; AAF10196.1;
                                                                                                                                                                                                                                   MEDLINE=20036896; PubMed=10567266; White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Elsen D.H., Gwin M.L., Nelson W.C., Richardson D.L., Dodson R.J., Haft D.H., Gwin M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Woffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U1-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein DR0609.
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Submitted (MAR-1998) to the
EMBL; Y14657; CAA74987.1;
EMBL; AJ225061; CAA12392.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=FRUIT BODY;
Asgeirsdottir S.A., (
Submitted (AUG-1997)
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Agaricales; Pleurotaceae;
NCBI_TaxID=5322;
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SMART; SM00075; HYDRO; 1.
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SEQUENCE 16
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                                                                                                                               TIGR;
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                                                                                                                                                                                                                "Genome sequence of the radioresistant bacterium Deinococcus
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	Search completed: April 21, 2003, 19:18:35 Job time : 94.5 secs	Qy 107 GGCACCGGCAAATCCACGCTGGCG 130 	US-09-513-151-3 (1-2041) x Q9RWQ7 (1-162)	Percent Similarity: 100.008 Best Local Similarity: 100.008 Query Match: 1.218 DB: 16
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Command line parameters:

-MODEL-frame+_n2p.model -DEV*xlh
-Q-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141246_27211/app_query.fasta_1.2183
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-DB-SwissProt_40 -QFMYF-fastan -SUFFIX-olin2p.rsp -MIMMATCH+0.1 -LOOPCL=0
-DOPEXT=0 -UNITS=bits -START=1 -END--1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALICN=200 -THR_SCORES-quality -TH_MIN=1 -ALICN=15 -MODE=LOCAL
-OUTFMY-pto -NOMM-ext -HarbSIZE=500 -MILLEN=0 -MAXLEN=2000000000
-USER-US09513151_@CGN_1_1_22_@runat_15042003_141246_27211 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPEXT=7
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01.NOV-1997 (Rel. 35, Last sequence update)
16.OCT-2001 (Rel. 40, Last annotation update)
Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D).
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Q39615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
                                                           between
                                                                                                                                                                                                                                                                                                                                     MEDLINE-97033539; PubMed-8879236;
                                                                                                                                                                                                                                                                                                                                                         STRAIN-CC-406
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Physiol. 107:1485-1486(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                    THYLAKOID MEMBRANE. SIMILARITY: BELONGS TO THE PSAD FAMILY
                                                                                                                                                           SUBCELLULAR LOCATION: ASSOCIATED WITH STROMAL SIDE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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ACYO_CHICK
YD22_MYCTU
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DVA1_DICVI
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UVRB_THETH
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Y253_THEMA
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R33A_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-513-151-3 (1-2041) x PSAD_CHLRE (1-196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD5_YEAST STANDARD; PRT; 428 AA. P07884; Q12203; 01-AUG-1988 (Rel. 08, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) tRNA isopentenyltransferase (EC 2.5.l.8) (Isopentenyl-diphosphate: tRNA isopentenyltransferase) (IPP transferase) (IPPT).
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=87172703; PubMed=3031457;

Majarian D., Dihanich M.E., Martin N.C., Hopper A.K.;

"DNA sequence and transcript mapping of MOD5: feature, region which suggest two translational starts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X79674; CAA56122.1; -.
EMBL; X74419; CAA52440.1; -.
InterPro; IPR003685; PsaD.
Pfam; PF02531; PsaD; 1.
                                                                                                                                                Slusher L.B., Gillman E.C., Martin N.C., Hopper A "mRNA leader length and initiation codon context
                                                                                                                                                                                                                          Cheret G., Bernardi A., Sor F.J.;
"DNA sequence analysis of the VPH1-SNF2
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities re
or send an
 ALTERNATIVE INITIATION, MEDLINE-94187700; PubMe
                                                                       Gillman E.C., Slusher L.B., Martin N.C.,
                                                                                                                                     alternative AUG
                                                                                                                                                                         ALTERNATIVE INITIATION, AND SUBCELLULAR LOCATION MEDLINE=92052176; PubMed=1946403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photosynthesis; Photosystem I; Chloroplast; Transit peptide
                                                                                    ALTERNATIVE INITIATION, AND SUBCELLULAR MEDLINE-91203856; PubMed-1850093;
                                                                                                                                                                                                                                                                             STRAIN-S288c;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD5 OR YOR274W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSIT
                                                           "MOD5 translation initiation sites determine
                                                                                                                                                                                                                Yeast 12:1059-1064(1996).
                                                                                                                                                                                                                                                              MEDLINE=97051594; PubMed=8896271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 GTTGCAGCTAGGCCAGCGGCTCGGCGG 156
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                                    on of mitochondrial and cy
Biol. 11:2382-2390(1991).
                                                                                                                                                                                                                                                                                                                 Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 AA;
                                                                                                                       selection for the yeast gene MOD5."; d. Sci. U.S.A. 88:9789-9793(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s a license agreement (See http://www.isb-sib.ch/announce/
to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 7:185-191(1987).
 ATION, AND SUBCELLULAR LOCATION PubMed=8139535;
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Matches:
                                                cytoplasmic tRNA
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                                                                                                 LOCATION
                                                                                                                                                                                                                                       region
                                                           Hopper A.K.;
mine N6-isopentenyladenosine
                                                                                                                                                             Hopper A.K.;
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                                                                                                             UVRB_MYCLE
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                                                                       P57991;
16-OCT-2001
                                                                                                UVRB_MYCLE
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                                       16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
Excinuclease ABC
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-i- FUNCTION: RESPONSIBLE FOR THE MODIFICATION OF A37 TO ISOPENTENYL A37 OF BOTH CYTOSOLIC AND MITOCHONDRIAL TRNAS.
-i- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate LRNA containing 6-isopentenyladenosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M15991; AAA34785.1; -.
EMBL; X89633; CAA61780.1; -.
EMBL; Z75182; CAA99499.1; -.
PIR; A26717; A26717.
SGD; S0005800; MOD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
Mycobacterium leprae.
Bacteria; Actinobacteria;
                           UVRB OR ML1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO0174; miaA; 1. Transferase; tRNA processing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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-i- ALTERNATIVE PRODUCTS: TWO ISOFORMS MAY BE PRODUCED FROM
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-i- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boguta M.,
Hopper A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitochondrion;
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40, Last sequence up
41, Last annotation
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Actinobacteria (class); Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                            TRANSFERASE
                                                                                                                                                                                                                                                                                                                                                                                                                         BINDS ISOPENTENYLPYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR CYTOPLASMIC/NUCLEAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRNA ISOPENTENYLTRANSFERASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRNA ISOPENTENYLTRANSFERASE,
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                                                                                                                                                                                                                          (1-428)
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Conservative:
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                                                                                                                                                                                                                                                                                                                         Length:
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                                                                   update)
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           UVRB_MYCTU
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                                                                                                              US-09-513-151-3 (1-2041) x UVRB_MYCLE (1-698)
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Pfam; PF00271; helicase_C; 1.
Pfam; PF002151; UVR; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
TICRFAMS; TIGR00631; UVrb; 1.
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MEDLINE-21128732: PubMed-11234002:
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quall M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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or send a
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8
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"MASSIVE gene decay in the leprosy bacillus.";

Nature 409:1007-1011(2001).

Nature 409:1007-1011(2001).

CATALYZES THE EXCISION REACTION OF UV-DAMAGED NUCLEOTIDE SEGMENTS

PRODUCING OLIGOMERS HAVING THE MODIFIED BASE(S). UVRB STIMULATES

THE ATPAGE ACTIVITY OF UVRA IN THE PRESENCE OF UV-IRRADIATED

THE ATPAGE ACTIVITY OF UVRA IN THE PRESENCE OF UV-IRRADIATED
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Barrell B.G.;
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PROSITE; PS50151; UVR;
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HSSP; P56981; 1
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NCBI_TaxID=1769;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                        40
                                                                                                                                                                                                                                                                                                              response; Excision nuclease; DNA repair; ATP-binding;
                                                     CTCGGGGCCACGGCACCGGCAAATCC
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STANDARD;
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 PRT;
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Matches:
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InterPro: IPRO01410; DEAD.
InterPro: IPRO01550; Helicase_C
InterPro: IPRO01500; VorB.
InterPro: IPRO01943; UvrB/C.
InterPro: IPRO01943; UvrB/C.
InterPro: IPRO01943; UvrB/C.
InterPro: IPRO01943; UvrB/C.
InterPro: IPRO0270; DEAD; 1.
Pfam; PF00271; Helicase_C; 1.
SMART; SM00480; DEXDC; 1.
SMART; SM00480; HELICC; 1.
TIGREPAMS; TIGRO0531; Uvrb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 9829987; pubMed = 9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillngworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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15-JUL-1998
15-JUL-1998
15-JUN-2002
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15-JUL-1998 (Rel. 36, Last sequence u
15-JUN-2002 (Rel. 41, Last annotation
Exchauclease ABC subunit B.
UVRB OR RV1633 OR MT1669 OR MTCY01B2.
                                                                                                                                                                                                                                                 EMBL; Z95554; CAB08886.1; -. EMBL; AE007030; AAK45939.1; HSSP; P56981; 1D9X.
                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg Belcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                             TIGREAMS; TIGRO0631; uv PROSITE; PS50151; UVR;
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                                                                                                                                                                                                               TubercuList; Rv1633;
                                                                                                                                                                                                                                     TIGR; MT1669;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOUBLE-STRANDED DNA. IT ALSO ENHANCES THE ABILITY OF TO UV-IRRADIATED DUPLEX DNA (BY SIMILARITY). SUBUNIT: CONSISTS OF THREE SUBUNITS; UVRA, UVRB AND USUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE UVRB FAMILY.
              response; Excision nuclease;
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               DNA repair; ATP-binding;
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ATP (POTENTIAL).

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RESULT 6
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EMBL: AF277381; AAK17096.1; -.
InterPro; IPR001569; Ribosomal_L37e; 1.
Pfam; PF01907; Ribosomal_L37e; 1.
ProDom; PD005132; Ribosomal_L37e; 1.
PROSITE; PS01077; RIBOSOMAL_L37e; 1.
                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Q9C0T1;
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                        nidulans during sexual development.", Gene 262:215-219(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. PubMed=11179686;
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Eurotiales; Trichocomaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Emericella nidulans (Aspergillus nidulans).
Eukaryota: Fungi: Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jeong H., Cho G., Han K., Kim J., Min Han D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCT-2001 (Rel. 40, Last annotation ribosomal protein L37,
                                  GlyAlaArgGlyProGluAsnHis 92
                                                           GGTGCCCGTGGCCCCGAGAATCAC
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Aspergillus
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borvillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Hailo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic C.,
RA Kobayashi Y., Koetter P., Mazuda S., Mauel C., Medigue C.,
RA Kurita K., Lapida R.P., Mizuno M., Moest D., Nakai S., Noback M.,
RA Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Riger M., Rivolta C., Rocha E., Roche B., Rose M., Stale Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                  Nature 390:249-256(1997)
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J. Bacteriol. 176:1451-1459(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levin P.A., Losick R., "Characterization of a cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94156852;
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Bacteria; Firmicutes;
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P37471;
                                                                                                                                                                 FUNCTION: REQUIRED FOR VEGETATIVE AND SPORULATION SEPTUM FORMATION. REQUIRED FOR THE ACTIVATION OF GENES EXPRESSED THE CONTROL OF THE SPORULATION TRANSCRIPTION FACTORS SIGNATURE CONTROL OF THE SPORULATION TRANSCRIPTION FACTORS
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                                                                                                                                                                                                                            ECUTATION ATCC 35092 / DSM 1617 / P2;

X MEDLINE-21332296; PubMed=11427726;

X She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

A Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,

A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

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A Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

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15-JUN-2002 (Rel. 41, Last annotation
V-type ATP synthase subunit D (EC 3.6.
ATP DR SS00566.
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EMBL; D26185; BAA05297.1;
EMBL; Z99104; CAB11838.1;
SubtiList; BG10125; divIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charlebois R.I., Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C Confalonieri F., Curtis B., Duguet M., Erauso, G., Faguy D., Gaasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., Kushwaha N., van der Oost J., Young F., Zivanovic Y., Doolittle W.F. St Jean A., van der Oost J., Young F., Zivanovic Y., Doolittle W.F. Ragan M.A., Sensen C.W., Ragan M.A., Sensen C.W., the modern content and organization of a 281-kbp contig from the genome the extremely thermophilic archaeon, Sulfolobus solfataricus P2.":
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16-OCT-2001 (Rel.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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55948; PubMed=10701121;
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EMBL; AE006687; AAK40881.1; -
InterPro; IPR002699; ATPSynt_Dsub
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STRAIN-MOPN / Nig;
MEDLINE-20150255; PubMed-10684935;
MEDLINE-20150255; PubMed-10684935;
Meddine-C., Brunham R.C., Shen C., Gill S.R., Heidelberg
Read T.D., Brunham R.C., Shen C., Utterback T., Berry
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
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proDom; PD004122; ATPsynt_Dsub; 1.
TIGRFAMS; TIGR00309; V_ATPase_subD;
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TIGR; TCU/3;
InterPro; IPRO03136; Cytlayıw---
InterPro; IPRO03136; Cytlayıw---
Pfam; PPC0224; Cytldylate_kin; 1.
TIGRFAMS; TIGR00017; cmk; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
Transferase; Kinase; ATP-binding; GMP SIMILARITY).
74024 MW; 6013B4CDA7F6C59C CRC64;
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Cytidylate kinase (EC 2.7.4.14
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                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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Bacteria; Chlamydiales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequences of Chlamydia trachomatis MoPn and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=83560;
                                                                                                                                                                                                                                EMBL; AE002342; AAF39547.1;
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TC0737; -.
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2.7.4.14) (CK) (Cytidine monophosphate kinase)
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Salzberg
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MBL outstation .
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Alignment Scores:

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                                                                                                                                                         Pfam; PF02224; Cytidylate_kin; 1.
TIGRFAMS; TIGR00017; cmk; 1.
Transferase; Kinase; ATP-binding; Complete proteome.
NP_BIND 15
ATP (BY SIMILARITY).
SEQUENCE 216 AA; 24021 MW; A50CB216A90363C6 CRC64;
                                                                                                                                                                                                                                                modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                        EMBL; AE001319; AAC68052.1; HSSP; P23863; 1CKE.
                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: ATP + (d)CMP = ADP + (d)CDP.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: BELONGS TO THE CYTIDYLATE KINASE FAMILY. SUBFAMILY 1.
                                               107
                                                                                             Match:
                                                                                                                                   NO . .
                                                                                                                                                                                                                                                                                                                                                                                            Stephens R.S., Kalman S., Lammel C.J., Fa
Mitchell W.P., Olinger L., Tatusov R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia trachomatis.
Bacteria; Chlamydiales;
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                          Science 282:754-759(1998)
                                                                                                                                                                                                                                                                                                                                                                      Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-D/UW-3
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                         Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate intracellular pathogen Chlamydia trachomatis.";
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                        GlyThrGlyLysSerThrLeuAla 17
                                 GGCACCGGCAAATCCACGCTGGCG 130
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2.7.4.14) (CK) (Cytidine monophosphate kinase)
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01-NOV-1997
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                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical protein in tutB 3'region (Fragment).
Erwinia herbicola.
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                        Bacteria;
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PROSITE; PS00603; TK_CELLULAR_TYPE; FALSE_NEG.
Transferase; Kinase; DNA synthesis; ATP-binding; Complete
NP_BIND 9 16 ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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050519;
30-MAY-2000
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Nature 417:141-147(2002).
-i- CATALYTIC ACTIVITY: ATP +
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                        Proteobacteria;
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                                                                                                                                                                                                                                   STANDARD;
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            subdivision; Enterobacteriaceae;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-Goel / Gol / ATCC BAA-199 / DSM 3647 / OCM

MEDLINE-22120827; PubMed-12125824;

Deppenmeier U., Johann A., Hartsch T., Merkl R.,

Martinez-Arias R., Henne A., Wiezer A., Baeumer :

Brueggemann H., Lienard T., Christmann A., Boemer

Bhattacharyya A., Lykidis A., Overbeek R., Klenk

T-i+7.H.-J., Gottschalk G.;
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STRAIN-Goel / Gol / ATCC BAA-199 /
MEDLINE-98218550; PubMed-9559648;
                                                                                                                                                                                                                                                                                                                                                                   15-JUN-1999 (Rel. 38, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tetrahydromethanopterin S-methyltransferase sı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U25347; AAA66392.1; -
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                                                                                                                                                                methyltransferase of
                                                                                                                                                                             *Cloning, sequencing and expression of the genes encoding translocating N5-methyltetrahydromethanopterin:coenzyme
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Pfam; PF01232; Mannitol_dh; 1.
PROSITE; PS00974; MANNITOL_DHGENASE; PARTIAL
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                            Klenk H.-P., Gunsalus R.P.,
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                                                                                                                                                                                                                                                                                                                               Query
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                                                                                                                                                                                                                                                                                                                                                                   Score:
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                                                                                                                 Ul-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADH pyrophosphatase (EC 3.6.1.-).
NUDC OR H10432.
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome of Methanosarcina mazel: evidence for lateral getransfer between Bacteria and Archaea.";
J. MOI. Microbiol. Biotechnol. 4:453-461(2002).
-i- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE METHANOGENESIS, THE FORMATION OF METHYL-COENZYME MAND METHANOFMETHANOPTERIN FROM COENZYME MAND MS-METHYL-TETRAHYDROMETHANOPTERIN. THIS IS A ENERGY-CONSERVING, SO
SEQUENCE FROM N.A.
STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., Whi
Kerlavage A.R., Bult C.J., Tomb J
                                                                                                                                                                                                          HAEIN
                                                                                                                                                                                                                                                                    1034, GCACGATTTCAAGAGCAGGTTCAA 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                             NUDC_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
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                                                                        NCBI_TaxID=727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: BINDS 5-HYDROXYBENZIMIDAZOL COBAMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin +
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232
16
71
71
127
161
240
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85 85 85 S-HYDROXYBENZIMIDAZOL
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                                                                                                gamma subdivision; Pasteurellaceae;
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G -> R (IN I
N -> D (IN I
E -> G (IN I
D -> E (IN I
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            White O.,
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N -> D (IN REF. 1).
E -> G (IN REF. 1).
D -> E (IN REF. 1).
44C086DD3561E526
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Indels:
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  Dougherty
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ZOL COBAMIDE
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SCIENCE 269:496-512(1995).
-I- CATALYTIC ACTIVITY: NADH + H(2)O = AMP + NMNH.
-I- COFACTOR: REQUIRES DIVALENT IONS: MANGANESE OR MAGNESIUM
-I- COFACTOR: REQUIRES DIVALENT TONS: MANGANESE OR MAGNESIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NRZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Whole-genome random sequencing and assembly of Haemophilus inf
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
1-acyl-sn-glycerol-3-phosphate acyltransferase delta (EC 2.3.1.51)
AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphatidic acid
AGP acyltransferase 4) (1-AGPAT 4) (Lysophosphate 0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                      acyltransferase-delta) (LPAAT-delta) (1-acylglycerol-3-phosphate 0-
Strausberg
                                 TISSUE-Spleen;
                                                                                                                Submitted (JUN-1999)
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00502; NUDIXFAMILY.
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                                                            SEQUENCE FROM N.A.
                                                                                                                                                 "Structure and
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                                                                                                                lysophosphatidic acid acylt EMBL/GenBank/DDBJ databases
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Matches:
Conservative:
Mismatches:
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RESULT 15
YPZ8_CAEEL
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01-FEB-1996
15-JUL-1999
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P98061;
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            the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                        Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel.
15-JUL-1999 (Rel.
Hypothetical zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF156776; AAF80338.1; -.
EMBL; BC020209; AAH80209, 1; -.
INTERPO, IPRO02123; Acyltransferase.
Pfam; PF01553; Acyltransferase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: CONVERTS LYSOPHOSPHATIDIC ACID (LPA) INTO PHOSPHATID ACID BY INCORPORATING ACYL MOIETY AT THE 2 POSITION (BY SIMILARITY).
-:- CATALYTIC ACTIVITY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate.
CoA + 1,2-diacyl-sn-glycerol 3-phosphate.
                                                                                                                                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                    F42A10.8
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                                                                                                                                                                         Latreille P.;
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(Rel. 33, Last sequence update)
(Rel. 38, Last annotation update)
, l zinc metalloproteinase F42A10.8
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Pred. No.:
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HSSP; P28875; 11AF.
MEROPS; M12.UPA; -.
WormPep; F42A10.8; CE01299.
UnterPro; IPR001506; Astacin.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000561; EGF-11Ke.
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PROSITE; PS01180; CUB; 1.
PROSITE; PS01022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
Hypothetical protein; Repeat; Hydrolase; Metalloprotease; EGF-like domain; Zinc; Signal.
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Command line parameters:

MODEL-frame+_n2p.model -DEV=xlh
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-Q-/cgn2_1/USBTQ_Spool/US09513151/runat_15042003_141247_27235/app_query.fasta_1.2183
-DB-PIR_73 -OFMT-fastan -SUFFIX-olinp.rpr -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-olinp -TRANNS-human40.cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-quality -TH_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto
-NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
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-USER-US09513151_@CGN_1_1_52_@runat_15042003_141247_27235 -NCPU-6 -ICPU-3
-USER-US09513151_@CGN_1_1_52_@runat_15042003_141247_27235 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NGE_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-MARN_TIMEOUT-30 -THREADS-1 -XOAPOP-60 -XOAPEXT-60 -FGAPDD-6 -FGAPEXT-7
-YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7
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## psaD protein - Chlamydomonas reinhardtii C;Species: Chlamydomonas reinhardtii C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999 C;Accession: S47088 R;Farah, J.A.; Frank, G.; Zuber, H.; Rochaix, J.D. submitted to the EMBL Data Library, June 1994 A;Description: Cloning and sequencing of a cDNA encoding the photosystem I PsaD s A;Reference number: S47088

ALIGNMENTS

Query Match: Percent Similarity: Best Local Similarity: Alignment Scores: Score: Pred. No.: 3.84 9.00 100.00% 100.00% 1.36% Mismatches: Indels: Conservative: Matches: 196 0 0

A;Molecule type: mRNA A;Residues: 1-196 <FAR> A;Residues: 1-196 <FAR> A;Cross-references: EMBL:X79674; NID:g498823; PIDN:CAA56122.1; C;Superfamily: photosystem I chain II

PID: 9498824

A; Status: preliminary A; Accession: S47088

## US-09-513-151-3 (1-2041) x S47088 (1-196)

δõ B 130 GTTGCAGCTAGGCCAGCGGCTCGGCGG 156 21 ValAlaAlaArgProAlaAlaArgArg 29

C;Species: Pseudomonas aeruginosa (;Date: 06-Sep-1996 #sequence_revision 13-Mar-1997 #text_change 24-Oct-2000 C;Accession: S54702; B83595 C;Accession: S54702; B83595 R;Whitchurch, C.B.; Mattick, J.S. twitching motility protein PilU PA0396 [imported] - Pseudomonas aeruginosa (strai

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A:Note: the nucleotide sequence C:Genetics:
A:Gene: SGD:MOD5
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R; Najarian, D.; C
Cell. Biol.
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A:Residues: 1-428 <CHE>
A:Cross-references: EMBL:275182; NID:g1420613; PID:e252418;
A:Experimental source: Strain S288C
                                                                                                                                                                     A;Title: DNA sequence analysis of the VPH1-SNF2 region on chromosome A;Reference number: S72039; MUID:97051594; PMID:8896271 A;Accession: S72045
                                                                                                                                                                                                                                                                                                                                                         A;Title: DNA sequence and transcript mapping of MOD5: features A;Reference number: A26717; MUID:87172703; PMID:3031457 A;Accession: A26717
                                                                                                   A; Molecule type: DNA
A; Residues: 1-428 <CI
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A; Residues: 1-374, 'R', 376-428 <NAJ>
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Nature 406, 959-964, 2000
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A; Residues: 1-382 <STO>
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A;Title: Characterization of a gene, pilU,
A;Reference number: S54702; MUID:95157252;
A;Accession: S54702
A;Status: preliminary
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Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000;
Accession: S67176; A26717; S72045
                                                                                Cross-references:
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                                                EMBL:X89633; NID:g1279694; PIDN:CAA61780.1; PID:g14. de sequence was submitted to the EMBL Data Library.
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Conservative:
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K.; Lim,
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A;Gene: uvrB
C;Superfamily:
                                         A; Experimental C; Genetics:
                                                                                                               A; Molecule type: DNA
A; Residues: 1-698 <COL>
                                                                                                                                                                                 A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Bar A;Title: Deciphering the biology of Mycobacterium tuberculosis from A;Reference number: A70500; MUID:98295987; PMID:9634230 A;Accession: G70559
                                                                                                                                                                                                                                                                         R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davles, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                      probable uvrB protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 *sequence_revision 17-Jul-1998 *text_change 02-Feb-2001
                                                                                          A; Cross-references:
                                                                                                                                                      A; Status: preliminary; nucleic acid sequence
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source:

strain

H37Rv

GB: Z95554;

GB:AL123456;

NID: g3261771;

PIDN:CAB08886.1; PID:g21

not

shown;

translation

not

Barrell,

N.; Holro

the

complete B.G

excinuclease

ABC

chain

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Score:
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T38664
                                                         US-09-513-151-3 (1-2041) x T38664 (1-434)
                                                                                                        Best Local Similarity:
Query Match:
                                                                                                                                        Percent Similarity:
                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-434 <MUR>
                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z21804
A; Accession: T38664
                                                                                                                                                                                                                                                                                                                                                                    R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-513-151-3 (1-2041) x S67176
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                                                                                                                                                                                                                                                              A;Experimental source: strain
                                                                                                                                                                                                                                                                               A;Cross-references:
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LysileProlleValValGlyGlyThr
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Matches:
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C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: D81432
R;Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillir C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: E87082
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C;Species: Mycobacterium leprae
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A; Accession: D81432
A; Status: preliminary
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A; Residues: 1-698 <STO>
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A; Experimental C; Genetics:
             A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                              hypothetical protein Cj0148c [imported] - Campylobacter jejuni (strain NCTC 11168)
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Best Local Similarity:
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                                                      A; Residues: 1-112 <PAR>
                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Genetics:
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S.; Feltwell, T.;
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Matches:
Conservative:
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Indels:
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Fraser, F
                                     PIDN:CAB72632.1;
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A.; Hamlin, N.;
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                                     PID: g69676
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A;Title: Systematic sequencing of the 180 kilobase region of A;Reference number: S65967; MUID:96051385; PMID:7584024 A;Accession: S66092
                                                      A;Cross-references: GB:L23497; NID:g469178; R;Ogasawara, N.; Nakai, S.; Yoshikawa, H. DNA Res. 1, 1–14, 1994
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                                                                                                               A; Molecule type: DNA
A; Residues: 1-125 <LEV>
                                                                                                                                                                    A; Reference number: A; Accession: B53380
                                                                                                                                                    A;Status: preliminary
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M.; Ohtuku, Y.; Funalidani, ...
M.; Ohtuku, Y.; Funalidani, ...
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome
A:Deference number: A71000; MUID:98344137; PMID:9679194
A:Deference number: A71000; MUID:98344137; PMID:9679194
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Best Local Similarity:
Query Match:
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C;Superfamily: (
                                                                C; Species: Bacillus subtilis
C; Date: 23-Mar-1995 #sequence_revision
C; Accession: B53380; S66092; A69616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
C:Accession: C71104
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C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: this accession replaces C;Genetics:
 A; Title: Characterization of a cell division A; Reference number: A53380; MUID: 94156852; PN
                                                                                                               cell division initiation protein divIC -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP000004; NID:g3236131; A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-121 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PH1094 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
                                                 R; Levin, P.A.; Losick, R
                                                                                                                                                                                                                                                 US-09-513-151-3 (1-2041) x C71104 (1-121)
                                   Bacteriol. 176, 1451-1459, 1994
                                                                                                                                                                                                                 1111 ACTICTCTTGTTCTCAGCTTCATT
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Tanaka, T.; Kudoh, Y.; Yamazaki,
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PMID:8113187
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PIDN: AAB38379.1;

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A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel R.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Schrieter, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001919; GB:AE000513; NID:g6458307; PIDN:AAF10196.1; PID:g64583A;Experimental source: strain R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Genome sequence of the radioresistant bacterium Deinococcus A; Reference number: A75250; MUID:20036896; PMID:10567266 A; Accession: C75497
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C;Superfamily: Bacillus subtilis cell division initiation protein divIC
                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein - Deinococcus radiodurans (strain R1)
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A;Experimental source: strain 168
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A; Residues: 1-125 <KUN>
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
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A;Molecule type: DNA
A;Residues: 1-125 <OGA>
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A:Reference number: Z21592
A:Accession: T35881
A:Status
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C; Keywords:
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R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rayandream, M.A submitted to the EMBL Data Library, November 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thymidine kinase (EC 2.7.1.21) [similarity] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002
                                                                                      Percent Similarity:
Best Local Similari
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C:Superfamily: Escherichia coli thymidine kinase
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A; Residues: 1-216 <OLI>
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US-09-513-151-3 (1-2041) x T35881
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Best Local Similarity:
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A; Residues: 1-213 <KUR>
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A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track; Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: G71512
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C;Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 08-Oct-1999
C;Accession: G71512
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind,
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind,
Science 282, 754-759, 1998
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81670
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A: Residues: 1-216 <ARN>
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Query Match:
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A;Experimental source: strain Nigg (MoPn)
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Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; GB:AE001273; NID:g3328881; PIDN:AAC68052.1; PID:g332888
D, strain UW-3/Cx
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R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K. awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 199
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE2361 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: F72464
                                                                                                                                                                                                                                                                                                                                                                       A;Gene: APE2361
C;Superfamily: peroxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:AP000064;
A;Experimental source: strain K1
                                                                                                                                                               US-09-513-151-3 (1-2041) x F72464 (1-246).
                                                                                                                                                                                                          Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-246 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: F72464
               Search completed: April 21, 2003, 19:21:02
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Best Local Similarity:
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Job time : 51 secs
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601860153F1 NIH_MGC_61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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Mammalia; Eutheria;
1 (bases 1 to 711)
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BG506209
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: CLONETECH Laboratories, cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                       224
                                                 Library."
a 145 c
                                                                                                                                                                 /tisue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'
Sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3'
Average
                                                                                 (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                              /clone_lib="NIH_MGC_61"
                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4072428"
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
29.1%;
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Primates;
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GAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACATGTCC
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                                                                             TGAGGATCTTCTTGTGGTGAATACCAGGATTGACTGCATCCCTTTAAAAGAAGTTTTAT 1703
                                                                                                                                                                         AGCTCCTTGTGTGGCTGATGTGTC-TGGAAATGATGTAGTTCAGGAAAGCATTTTTTTTT 158
                                                      TGAGGATCTACTTGGAGGTGAATACCAGGATTGACTGCATCCCTTTTAAAGAAG-TTCAT 658
                                                                                                         ACTTTGAACCTTAAAGGTTCTATTCATTAAAAAGCAGCAAAGATTCCACATATTAATACA
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Search completed: April Job time: 3858.56 secs 21, 2003, 18:21:11

Query Match

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CATAGGACTTGAAGACCAAAGACTTTGAAATTTGCGAGCTGCTCATGTGTGAGTTATTAT 1958
                                                                                                 AACCAAACTAGTTCTCGGAATTCTACAGAGAAGGAGGGGAATCAGACTGAGGAAGCTGTGA 1898
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/lab_host="DHIDB (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: ECRR I; Site_2: Not I;
NCI_CGAP_EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
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TAG_SEQ-ACACTTGCAC"
128 c 97 g 195
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/dev_stage="Adult"
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AV759288 MD:
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Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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This clone is available at CHGC
Thocation/Qualifiers
1. 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiII
/note="Vector: pTriplEx2; Site_1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MDSBLH01"
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                                                            mRNA sequence.
BG034660
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10089 row: 1 column: 05
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1 (bases 1 to 772)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                   224
                                                                                                                          Conservative
                                                                                                                                                                                               /clone="IMAGE:4394260"
/clone=lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 155 c 178 g 214 t 1 others
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/db_xref="taxon:9606"
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Pred. No. 1.1e-115;
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Email: Capabs-remail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LINL at: http://image.linl.gov

The following repetitive elements were found in this CDNA

sequence: 1-36, >POLY_A#Simple_repeat (matched compliment)
                                                                                                                                        Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 624)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Proj
                                                                                                                                                                        Tumor Gene Index
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                                                                                               mRNA sequence.
BI161353
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 2.4e-123;
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                                                                                                                              GAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCC
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLCM1835 row: f column: 16
High quality sequence stop: 734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:5019663"
/clone=lib="NIH_MGC_42"
/tissue_type="epithelioid carcinoma cell line"
/tissue_type="epithelioid carcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: poTB7; Site_1: XhoI;
Site_2: EccRI; cDNA made by oligo-dT priming.
Directionally cloned into EccRIXhoI sites using the
following 5' adaptor: GGCACAGA(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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Pred. No. 4.4e-123;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCATAGAAAGTCAGAGTGTTTCCCCAGACTATAACAAAGAACCTAAAGGGAAGGGATC 1296
                       GTGGTTTTAAAGTCTCACGTTCTCTATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTG 1536
                                                                                                                                                                                      AAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTCCCACCATTTTCTTTTGAT 1470
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                                                                      GTGGTTTTAAAGTCTCACGTTCTCTATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTG
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Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics (www.resgen.com).
Seq primer: M13 Reverse.
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: 319 335 9565
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//lab_host="mild" (Life Technologies) (Ti phage resistant)"
//lab_host="mild" (Per vector: pT7T3-Pac (pharmacia) with a modified polylinker; Site_1: Not I;
UI-E-EDI is a normalized cDNA library containing the following tissue(s): fetal eye. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGCGTATACC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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/dev_stage="fetal"
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/clone_lib="UI-E-E01"
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/db_xref="taxon:9606"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602640078F1 NIH_MGC_61 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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    259
                                                                 /tissue_type="embryonal carcinoma"
//lab_host="DHHOB (T] phage-resistant)"
/note="organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="organ: pDNR-LIB (Clontech); Site_1:
/note="organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
/note="organ: pDNR-LIB (Clontech)
                                        Library."
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/clone="IMAGE:4771338"
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AI133396.1
                                                                                                                                                                               Expression profile analysis of a human fetal liver cDNA library Unpublished (1998)
Contact: Yongtao Yu
Department of Hematology
                                                                                                                                                                                                                                  Yu,
                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                  AI133396
HA2003 Human
                                                                                                                                         Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
                                                                                                                                                                                                                         and He, F
                                                                                                                                                                                                                                                                                   numan.
                                                                                                                                                                                                                                           mmalia; Eutheria; (bases 1 to 725)
                             220
                                                                                                                               yyt48@yahoo.com
                                                                                                                                                                                                                                Zhang, C.,
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human fetal liver cl
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/P3"
                            /note="Vector:
177 c 1:
                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                       GI:6360712
                                                                                                                                                                                                                                                                                                                                   fetal liver
33.7%;
                                                                                                                                                                                                                                Luo, L.,
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                           r: pCDNA1"
Score
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SOURCE
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BM721352
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AUTHORS
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                                                                    Bonaldo, M.F.,
                                                                                                          Homo sapiens
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1274 AAAGAACCTAAAGGGAAGGGAT-CCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGT 1332
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BM721352
Contact: Soares, MB
Program for Rat Gene
University of Iowa
                                                   Genome Res. 6 (9),
97044477
                                                                                                                                       Mammalia; Eutheria;
1 (bases 1 to 724)
                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                        Normalization and
                                                                                                                                                                                                                                                 GI:19041207
                                                                                                                          Lennon, G. and
                                                                                                        subtraction:
                                                                     791-806
                                                                                                                                                           Chordata;
Primates;
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                    Discovery
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); Mismatches
                                                                     (1996)
                                                                                                                        Soares, M.B.
                                                                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae;
                    and
                                                                                                        two
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Homo sapiens
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GAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTCCCACCATTTTCTTTTGATGTGG 1480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGGTGGTGGGGATCCAGTTCAGGAGGGAGGGGTATGTTTGTCTCCCCAGTCTGGGCAAAG 1420
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                                                                          TAGGACTTGAAGACCAAAGACTTTGAAATTTGCGAGCTGCTCATGTGTGAGTTATTATCA
                                                                                                                  TAGGACTTGAAGACCAAAGACTTTGAAATTTGCGAGCTGCTCATGTGTGAGTTATTATCA 1960
                                                                                                                                                                      CCAAACTAGTTCTCAGAATTCTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACA
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/note="Organ: Lung; Vector: pT7T3-Pac (pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-ENI is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAG_SEQ-CTGCTCAGGT"
172 c 116 g
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99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 727.4; DB 14;
Pred. No. 1.4e-135;
0; Mismatches 1;
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1961

268

GGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGAT 327

BASE CONTIGIN

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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National Institutes of Health, M
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Mammalia; Eutheria;
1 (bases 1 to 725)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="adenocarcinoma cell line"
/lab_host="bHi0B (phage-resistant)"
/lab_host="bHi0B (phage-resistant)"
/note="Organ: ovary; Vector: pOTB7; Site_1: xhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5;
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
Callfornia, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
86 a 175 c 197 g 167 t
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/clone="IMAGE:3141643"
/clone_11b="NIH_MGC_9"
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Pred. No. 3.3e-128;
0; Mismatches 14;
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les 785; Conserv
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                                                                                                                                                                                                                                        TTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGATGCCATACAATGAAGCTGA 1098
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ACCTAMAGAGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGA
                                                          ACCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGA 1338
                                                                                                                                                                                                                                                                                                        ATCTGATGTCTCGAAGTGGGAAGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAG
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                                                                                                                    GGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACCATAACAAAGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AGENCOURT_6416157 NIH_MGC_71
5', mRNA sequence
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Plate: LLAM12212 row: j column: 17
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Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/tissue_type="letiomyosarcoma"
/tissue_type="letiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1:
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1:
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1: pCMV
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/db_xref="taxon:9606"
/clone="IMAGE:5531248"
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95.7%;
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2024 University of I
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                   Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Club Sequencing by: Dr. M. Bento Soares, University of Iowa
Club Sequencing by: Dr. M. Bento Soares, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM975520 743 bp mRNA linear EST 21-MAR-2002 UI-CF-EN1-acw-c-07-0-UI.sl UI-CF-EN1 Homo sapiens cDNA clone UI-CF-EN1-acw-c-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                    Genetics (www.resgen.com).
The following repetitive elements were found sequence: 1-56, >AT_rich#Low_complexity (match
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                                                                                                                                                   Seq primer: M13
POLYA=Yes.
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1 (bases 1 to 743)
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                                                                                                                                                                                                                                           Clone Distribution: Researchers may obtain clones from
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acv-c-07-0-UI"
/clone_lib="UI-CF-EN1"
/tissue_type="Primary Lung CysticCells"
                                                                                                                                location/Qualifiers
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                                                                                    cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11486 row: e column: 04
                                                                                                                                                                                               1 (bases 1 to 799)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                                                                                                                                                                                                          mRNA sequence
BI758117
                                                                                                                                                                                                                                                                                                                           BI758117 799 bp mRNA linear EST 25-SE 603023811F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194347
                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                              BI758117.1 GI:15749695
                                                   quality sequence start: 2 quality sequence stop: 775.
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194347"
/clone_lib="NIH_MGC_114"
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207
       a
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV-Site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
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37.38;

DB 13;

Length

TACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATG AGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTG AAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACC AGACGCTATAATCAGAAGAA AATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTGCCCCTTGGAGGTCCTCTGAAGT GAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGG ACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACCTTCAGAAATA 311 AAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACC TGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATG TGCAGCTAGGCCAGCGGCGCGCGGGAGATCGTCAGCGCTGACTCCATGCAGGTCTATG 191 GGACCCTACCTCTTGTAGTGATTCTCGGGGGCCACGGGCACCCGGCAAATCCACGCTGGCGT GGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGT 131 ATAAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTT-GGAGGAACTAAGAGATTTTCAC 790 **AATTACTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGT** ACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTG ACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTG GAGCAACTGCTCTGATTGAAGATATTTTGCCCGAGACAAAATTCCTATTGTTGTGGGAG ACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATA Conservative 810 0, Score 760.8; DB 13 Pred. No. 2.9e-142; 0; Mismatches 2; Indels ω ,, Gaps 120 731 718 671 611 371 778 658 598 538 551 479 491 419 431 359 300 240 251 180 'n

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CTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGATG

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                                                                                                                                                                       CTACAGAGAAGGAAGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGAC-CAAAG
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                                                                                                                          CTGAAATGCAGCGTTTAAAAAACTTGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAG
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                                                       TTCAGGAGGGAGGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTC
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Email:
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1 (bases 1 to 987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Lidang Life Technologies. Contact: Feng Lidang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
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/lab_host="DH10B"
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/clone="CSODD008YN11"
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Fleischmann,W., Gaasterland,T., Gissl.C., King,B., Kochiwa,H.,
Kuehl,P., Lewis,S., Matsuov,Y., Nikaido,I., Pesole,G.,
Quackenbush,J., Schriml,L.M., Staubll,F., Suzukl,R., Tomita,M.,
Wagner,L., Washlo,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
Marchionni,L., Mashlma,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
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RingyB., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
Toyo-oka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L.,
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
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Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA library was prepared and 
Encyclopedia Project of Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) further details.
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                                                                                                                                                     /organism="Mus musculus"
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/db_xref="FANTOM_DB:3310075G14"
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                                                                                                          /db_xref="taxon:10090"
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  /dev_stage="adult"
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                                          /tissue_type="tongue"
/clone_lib="RIKEN ful
                                                                                       /sex="male"
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/db_xref="MGD:MGI:1914216"
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Query Match Best Local Similarity 76./ a 52.4%; 76.7%; Score 1069.6; DB 1 Pred. No. 3.5e-204; 525 g DB 11; Length

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CAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATC ACCCTGGCTCTGCAGTTAGGCCAGCGGCTCGGCGGCGAGATCGTCAGCGCCGACTCCATG ACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATG GGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCC GGCCTGCGGCGAACACTGCCACTTGTAGTGATTCTCGGGGGCTACTGGGAACTGGCAAGTCC 181 124 184

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 Kawai, J., Shinagawa, A., Arakawa, T., Hara, A., Fu
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Mus musculus adult male tongue cDh
Library, clone:2310075614:homolog
TRANSFERASE, full insert sequence
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submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Query Match
Best Local Similarity
488 CTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCA-547
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                                                                                                     CAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGT 487
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VDDMLAAGLLEELRGFHRRYNLKNISENSQDYQHGIFQSIGFKEFHEYLTTEGKCTPE
TSNQLLKKGIEALKQVTKRYARKQNRWYKNRFLSRPGPSVPPVYGLEVSDVSKWEESV
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/translation="MGTGKVVDRKVELEKEDGHELHKRLSQVDPEMAAKLHPHDKRKV
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                                                                                                                Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                           Mus musculus (strain:C57BL/6J) 18 days embryo cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1110007017.
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Mus musculus 18 days embryo whole body cDNA, RIKEN full-len
enriched library, clone:11110077017:homolog to TRNA
ISOPENTENYLPYROPHOSPHATE TRANSFERASE, full insert sequence.
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AIT18450 as56a07.x
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BE965936 601652530
AI749267 at41e07.x
AII93562 qe70f07.x
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BG575745 602597234
BG495857 602540248
BF064275 7457033.x
BI462398 603203761
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

genes

HTC 19-JAN-2002 full-length

NUMBER OF SEQUENCES: 1

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PUBLICATION DATE: RELEVANT RESIDUES US-09-075-904-1
Query Match 1.8%; Score 36.4; DB 2; Best Local Similarity 49.0%; Pred. No. 10; Matches 97; Conservative 0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 50341
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CELL LINE:
ORGANELLE:
ORGANELATE SOURCE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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ORIGINAL SOURCE:
ORGANISM: L5 mycobacteriophage
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PRIOR APPLICATION NUMBER: 08/247,901
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MEDIUM TYPE: 3.5 inch 1.44 MEDIUM TYPE: 1BM PC Compatible
COMPUTER: IBM PC Compatible
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IDENTIFICATION METHOD:
OTHER INFORMATION:
BLICATION INFORMATION:
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SOFTWARE: Word Processor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/075,904 FILING DATE: May 11, 1998
                                                                                                                         FILING DATE:
                                                                                                                                       DOCUMENT NUMBER:
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TISSUE TYPE:
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DEVELOPMENTAL STAGE:
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REFERENCE/DOCKET NUMBER: 96
TLECOMMUNICATION INFORMATION: (212) 697-5995
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(RANDEDNESS: single
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2298 TCGTGGCCGACAGCCGGG 2281
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Search completed: April 21, 2003, 16:30:04
Job time: 3773.69 secs

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Best Local Similarity
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MEDIUM TYPE: 3.5 inch 1.44 I
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                          APPLICATION NUMBER: 08/0 FILING DATE: April 29, 1 ATTORNEY/AGENT INFORMATION:
                                                                                        PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
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ZIP: 91320
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CITY: New York
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               REGISTRATION NUMBER:
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    Application US/08247901C
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                                                                                                                     May 23,
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96700/273
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Pred. No. 1.
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RESULT 15
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IMMEDIATE SOURCE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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ORIGINAL SOURCE:
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CELL LINE:
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RELEVANT RESIDUES IN SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
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IDENTIFICATION METHOD:
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Pred. No. 10;
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US-09-075-904-1/c

Sequence 1 Patent No.

1, Application US/09075904 5. 5994137

INFORMATION:

L5 SHUTTLE PHASMIDS

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Best Local
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GENERAL INFORMATION:
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FILING DATE: 1997-06-13
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LING DATE: 1997-08-22
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           Hoffmann Sommergruber,
Breitenbach, Michael
Kraft, Dietrich
Rumpold, Helmut
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Pred. No. 1
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US-09-053-374A-4
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                                     TITLE OF INVENTION: MANUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                               APPLICANT:
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HYPOTHETICAL:
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OPERATING SYSTEM:
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10036-2711
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Sequence 4, Application US/09053374A Patent No. 6462177 GENERAL INFORMATION:
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: hazel (Corylus sp.)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                             1919 GACTTTGAAATTTGCGAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTCTATTGA 1978
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NAME: Jones III, Harry C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        FILING DATE: 01-JUN-
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                          GATGTTGTAACTCGGAAGAATGCAAACTGAATGTTGTATTACTTTTTGCATATATACAAA 663
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/ENTION: Allergens of Alder Pollen and
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SYSTEM: PC-DOS/MS-DOS
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MAMMALIAN BLOOD LOSS-INDUCED GENE; KD312
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7,586 7,590	7,588 7,585	7,599	7,595	7,761	6,892	6,845	6,631	6,864	6,910	6,874	6,636			6,894	6,880	6,879	6,888	6,903	6,637	5,88	5,87	6,662	6,8/8	,000,000			5.889	5,877	5,886	3,974	3,315	3,672	3,313	3,312	3,669

APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11

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APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630

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APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22

APPLICATION NUMBER:

60/056,889

LING DATE: 1997-08-22

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FILING DATE: 1997-06 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1997-04-1 APPLICATION NUMBER: 60 FILING DATE: 1997-04-1

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60/048,974 60/043,315

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APPLICATION NUMBER: 60/043,672 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11

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60/043,312

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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 186 Human Secreted profit Pr
                                                                                                                                                      Sequence 193, Application US/09149476 Patent No. 6420526
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APPLICATION NUMBER: 60/047,590
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APPLICATION NUMBER: 60/057,650
FILING DATE: 1997-09-05
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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FILING DATE: 1997-08-
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FILING DATE: 1997-08-22
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56; Conserv
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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/056,892

APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

RAPPLICATION NUMBER: 60/047,599
ER APPLICATION NUMBER: 60/047,599
ER FILING DATE: 1997-05-23
LER APPLICATION NUMBER: 60/047,588
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FILING DATE: 1997-05-APPLICATION NUMBER: 6
FILING DATE: 1997-05-

60/047,586

APPLICATION NUMBER: 60/C

APPLICATION NUMBER: FILING DATE: 1997-08

1997-08-22

60/057,761

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APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/056,864 FILING DATE: 1997-08-22

60/056,631

60/056,845

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60/056,888 60/056,903 60/056,637

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APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 APPLICATION NUMBER:

60/056,662

LING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,878 FILING DATE: 1997-08-22

LING DATE:

1997-08-22

FILING DATE: 1997-00-20
APPLICATION NUMBER: 60/0
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60/056,880

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/056,894

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APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER:

1997-08-22

LING DATE:

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US-09-149-476-316
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: TYPE: DNA

: ORGANISM: Glycine max

US-09-452-239-21
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                                       GENERAL INFORMATION:
                                                       Sequence 316, Apparent No. 64205
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 1, Application Patent No. 6441272
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/453,323
CURRENT FILING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/452,239 CURRENT FILING DATE: 1999-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase
FILE REFERENCE: BB1284 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rafalski, Antoni J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fader, Gary M.
APPLICANT: Rosen et al.
FITLE OF INVENTION: 186 Human Secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: Ye, Zheng-Hua
ITLE OF INVENTION: MODIFICATION OF LIGNIN CONTENT AND COMPOSITION IN
ITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILE REFERENCE:
                                                                                                                                                                                                                                      1366 GTTTGAGCTGTATTCCGTGTTATTCCTCAATTCTCTCCCTAAGCAAGATATTAGCAGATG 1425
                                                                                                                                                                                                                                                            1945 GIGIGAGITATIATCACIGCIGICTITCIATIGAGITACAAAICTATATITITATIGAAG 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1507
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                                                                                                                                                               1426 ATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1462
                                                                                                                                                                                                   2005 TTTAAATAAAGAAAAATTTACAAGAAAAAAAAAAAA 2041
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                                                                          Application US/09149476
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61.9%;
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Pred. No. 0.62;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                              Length 1507;
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FILING DATE: 1998-03-06
APPLICATION NUMBER: 60/040,162
FILING DATE: 1997-03-07
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APPLICATION NUMBER: 60/043,569 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,311
                                                                                                        APPLICATION NUMBER: 60/043,568 FILING DATE: 1997-04-11
                                                             APPLICATION NUMBER: 60/043,314 FILING DATE: 1997-04-11
                                                                                                                                               APPLICATION NUMBER: 60/043,580 FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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PPLICATION NUMBER: 60/047,601
TLING DATE: 1997-05-23
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LING DATE: 1997-05
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05-23
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LING DATE: 1997-05
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RESULT 8
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Sequence 21, Application US/09452239
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R APPLICATION NUMBER: 60/057,650
R FILING DATE: 1997-09-05
R FILING DATE: 1997-09-05,884
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,669
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R FILING DATE: 1997-05-2.
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R FILING DATE: 1997-05-2.
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APPLICATION NUMBER: 60/049,610
FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,881
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-2
APPLICATION NUMBER: 60/056,664
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APPLICATION NUMBER: 60/
APPLICATION NUMBER: 60/
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,585
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FILING DATE: 1997-08-22
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l Similarity 67.9%;
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                                                                                                                                                                                                                             Score 38; DB 4; Pred. No. 0.56; 0; Mismatches
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APPLICATION NUMBER: 60/0 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/056,662 60/056,878

LING DATE:

PLICATION NUMBER: 60/056,872 LING DATE: 1997-08-22

FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,893
FILING DATE: 1997-08-22

APPLICATION NUMBER: 60/056,630

FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
FILING DATE: 1997-08-22

PLICATION NUMBER: 60/056,889

APPLICATION NUMBER: 60/056,886

APPLICATION NUMBER: 60/0 FILING DATE: 1997-06-06 APPLICATION NUMBER:

60/048,974 60/043,315

1997-04-11

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FILING DATE:

1997-04-11

60/043,312

APPLICATION NUMBER:

1997-04-1

60/043,669

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER: 60/043,671 FILING DATE: 1997-04-11

APPLICATION NUMBER: 60/043,311

1997-04-

APPLICATION NUMBER: 60/043,569

1997-04-1997-04-

NUMBER:

60/043,314

1997-04-11

APPLICATION NUMBER: 60/043,674

1997-04-

APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11

APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11

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APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

APPLICATION NUMBER: 6 FILING DATE: 1997-08-

60/056,845 60/056,631 60/056,864

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APPLICATION NUMBER: 60/ FILING DATE: 1997-08-22

60/057,761

APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22

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APPLICATION NUMBER: 60/056,888

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1997-08-22 1997-08-22

APPLICATION NUMBER: 60/056,910 APPLICATION NUMBER: 60/056,874 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,636 APPLICATION NUMBER: 60/056,911 FILING DATE: 1997-08-22

Gaps

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; HYPOTHETICAL: NG; ANTI-SENSE: NO; ORIGINAL SOURCE: ORGANISM: Home US-08-974-691-7
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                                                                                                                           Query Match
Best Local Similarity
Matches 66; Conserv
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                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                              1934 GAGCTGCTCATGTGAGTTATTATCACTGCTGTCTTTCTATTGAGTTACAAATCTATAT 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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            CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 TCACCAACAAGGTTTCTGCCCAAGAGCAG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 6 FILING DATE: 20-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLE OF INVENTION: Cloning and Characterization of Napsin MBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                       DPOLAGI.

JECULE TYPE: CD
                                                                                                                                                                                                                                                                                      STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pabst, Patrea L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                       GTGAAGCGCATGCGCGGGGTGGTCGCGGAGGTCCTGCTACCCAGTAAAAATCCACTAT 1855
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                                                                                                                                                                                                                                                                                                                 nucleic
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                                                                                                                                                                                                                                                                                                                              1910 base pairs
                                                                                                                                                                                                                                                                                                                                                                               404-873-8795
                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      CDNA
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                                                                                                                                                                                                                                                                                                   single
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                                                                                                                                              Score 40.8; DB Pred. No. 0.096;
                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           166
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                                                                                                                                                            DB 4;
                                                                                                                                   42;
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US-09-149-476-187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 64205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 187,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER
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                          APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
                                                         APPLICATION NUMBER: 60/
FILING DATE: 1997-05-23
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                                                                                       ILING DATE:
                                                                                                                                                                                                         PLICATION NUMBER: 60/047,598
LING DATE: 1997-05-23
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LING DATE: 1997-03-07
                                                                                                                  LING DATE:
                                                                                                                                                              PLICATION NUMBER: 60/047,582
                                                                                                                                                ING DATE
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                                                                                                                                                                                                                                                       CATION NUMBER:
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                                                                                   NUMBER: 60/
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NUMBER: 60/043,580: 1997-04-11
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                                                                       60/047,632
                                                                                                   60/047,612
                                                                                                                                60/047,596
                                                                                                                                                                                                                                                                                   60/047,587
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                                         60/047,601
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US-08-936-165A-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quence 65, Application US/08936165A tent No. 6348582
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 846 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
00/027,032
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     262 CTTTGTGGATCCTCTTGTGACCAATTACACA 292
                                                                                                                                                       142 CCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGA 201
                                                                                                                                                                                        214 TATTGTAGTAATTGTGGGGCCAACTGCTTCAGGTAAAACAGAGCTTAGCATAGAACTCGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 610-270-4478
                                                                                     202 CATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAATCTGCCGGCACCACATGATCAG
                                                                                                                    154 GAAGCGTATCAATGGTGAAATCATAAGCGGTGATTCTATGCAAGTTTACAAACATATGAA
                                                                                                                                                                                                                        82 TCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGG 141
                                                    94 TATTGGAACTGCACAAGTAACACCTGAAGAAATGGATGGTATTCCACATCATTTAATTGA 35
                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gimmi, Edward REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                             846 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                             Conservative
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Rosenberg, Martin
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onetto, Michael
                                                                                                                                                                                                                                                                                                                                               Genomic DNA
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534
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                                                                                                                                                                                                                                                                           Score 47.8; DB 4;
Pred. No. 0.00059;
                                                                                                                                                                                                                                                             Mismatches 102;
                                                                                                                                                                                                                                                                                            Length 846;
                                                                                                                                                                                                                                                             Indels
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US-09-221-017B-497
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US-09-221-017B-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6444799 GENERAL INFORMATION:
                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 497, Application US/09221017E
                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
4062 TAACGATCTTGGGGCCTACGGCATGCGGCAAGACTCGTCTGGCCGTAAGCCTCGCATATC 4121
                                                                                                                                                                                                             ANTI-SENSE: UNK
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
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                               87 TAGTGATTCTCGGGGCCACGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/221,017B FILING DATE: 23-DEC-1998
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CITY: Palo Alto
                                                                                                                                               NAME/KEY: misc_feature LOCATION: 1...5884
                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,4
REFERENCE/DOCKET NUMBER: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/
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FILING DATE: 09-APR-1998
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                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
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94304-1018
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                                                                                                                                                                                               PORYPHYROMONAS GINGIVALIS
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30-JAN-1998
                                                                                                                                                                                                                                                          DNA (genomic)
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N: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
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                                                                             Score 46.6; DB 4; Pred. No. 0.0037;
                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-103-840A-1/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAITITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                        3040576 AACTCGATGTCCTGGATGTCACCGAAACC---GCGACCGTGGCGCGCTACCAGCGGGCCG 3040520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
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                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           3040519 CCGCGGCGGACATCGAGGCGATCGCAGCCCGGGGAGCGGTGCCGGTCGTGGTGGGCGGCT 3040460
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                                                 APPLICANT:
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                        APPLICANT:
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  APPLICANT:
                                                                                                                                                                                                                                                                                            375 CCAATTATTACATTGAATCTCTGCTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  255 TGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAG 314
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nes 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAATATTTAGCTTCATTCGACAAAGAATCAGCCAAGGATATACATCCTAATAACAGAAA 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCGGCGGT--------GAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAG 194
                                                                                                                                                                                                                                                                                                                                                                                      CAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAA 374
                                                                                                                                                                                                                                             CGATGCTGTATGTCCAATCCCTGCTC 3040434
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DORNER, F. SCHEIFLINGER, F. FALKNER, F. G.
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Pred. No. 5.1e-05;
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                  1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               1329
                                                                                                                                                                                                                                                                                                                                                                                  1133 GATCGAATCATTGGGGATCGCGAATGGGCACCGCACATAAAATCCAAATCCCACTTG
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LENGTH: 7218 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1073 ATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: line:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Rei
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                              1193 AACCAACTGAAGAAAAGAAGAATTGGACTCAGATGCTGTCAACACCCATAGAAAGTCAG 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 26-AUC
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                                  GAATTCTCTGCATAGCAGAAAAGCTCCCA 1461
                                                                                                                                                                                                                                         AGTGTTTCCCCCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCCAGGGCAGAATGAT 1312
                                                                                                                                                                                                                                                                               ATCCAGTTCAGGAGGGGAGGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCG. 1432
                                                                                                                                       CAAGAGCTGAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGG 1372
                                                                                                                                                                                                            RRRRRRRRRRRRRRRRRRRRRATCGCA 1061
                                                                  12;
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1800 Diagonal Road
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Minimum DB
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1: /cgn2_6/ptodata/1,

2: /gn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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Match Length
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-149-476-187

US-09-149-476-131

US-09-149-476-131

US-09-149-476-123

US-09-149-476-123

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Sequence 1334, Ap
Sequence 1, Appli
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Sequence 316, Appli
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Sequence 123, Appli
Sequence 14, Appli
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; SEQ ID NO 1334
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Staphylococcus ep
US-09-134-001C-1334
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US-09-134-001C-1334

Sequence 1334, Application US/09134001C

Patent No. 6380370

Patent No. 6380370

PATENCE TO STAPPLICATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPPLICATE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE, GTC-097

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT ELING DATE: 1988-08-13

CURRENT FILING DATE: 1988-08-13
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Best Local
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                 142 CCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGA 201
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                                                                                                                                                                                                                                                                                    82 TCTTGTAGTGATTCTCGGGGCCACGGGCAAATCCACGCTGGCGTTGCAGCTAGG 141
                                                                                                                               CTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGC
                                                                                                                                                               TATTGGTACAGCAAAAGTTACAACTGAAGAAATGGAAGGTATACCACATTATATGATAGA
                                                                                                                                                                                                                  TAAAAAATTTAATGGAGAAATTATTAGCGGAGATTCAATGCAGGTCTATCAAGGAATGGA 143
         ATATATACAATCTCTCTTATACAACTATGCTTTTGAAGATGAATCCATATCTGAAGATAA
                            TTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCAC
                                                                          TCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTA
                                                                                                               TATTTTGCCTCCAGATGCTTCCTTTTCTGCATAT - - - GAATTTAAAAAAAGGGCAGAAAA
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                                                                                                                                                                                                                                                                    TITAATCGTTATTGTAGGTCCAACTGCTTCAGGTAAAACTGAGTTAAGTATTGAAGTTGC 83
                                                           ATATATTAAAGATATTACTAGAAGAGGCAAGGTGCCTATTATAGCAGGAGGAACAGGACT
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US-07-867-106-2
US-08-987-439-2
US-08-885-469-1
US-09-625-918-1
US-09-724-864-9
US-09-784-316-1
US-09-784-316-1
US-09-784-316-1
US-08-457-459-1
US-08-457-459-1
US-08-55-678-1
PCT-US95-02275-1
US-08-2824-757-1
US-08-2824-757-1
US-08-202-056-4
US-08-202-056-4
US-08-202-056-4
US-08-202-056-4
US-08-701-053A-3
US-08-701-053A-3
US-08-805-478-3
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Pred. No. 5,
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APPLICANT: Leder, Philip
APPLICANT: Leder, Philip
FITTLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
FITTLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
CURRENT APPLICATION NUMBER: US/09/835,232
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/196,811
PRIOR APPLICATION NUMBER: US 60/196,811
PRIOR PILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 180216
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                            Db 102368 GCGTGACTTATTTAATCTTGTGATTTTGTTCTGAGGTAGCTAATAATTTTATCATAACAA 102309
                                                                                                                                                                                                                                                                                                                   Db 102428 TTAGAAACCACTGACACATATAATGACTTTTCAAGATATTTAACTAGCTTTATAGGCTCCT 102369
Search completed: April 21, 2003, 18:47:42 Job time: 370.611 secs
                                                                                                           Db 102308 GATAAATTTTTAAGAAAATTATTGGAAAGTATGAA 102274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6
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US-09-835-232-6/c
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Best Local Similarity 53.5%;
Matches 83; Conservative
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Patent No. US20020098489A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                              1945 GIGTGAGITATTATCACIGCTGTCTTTCTATTGAGTTACAAATCTATATTTTTATTGAAG 2004
                                                                                                                                                             2005 TTTAAATAAAGAAAAATTTACAAGAAAAAAAAA 2039
                                                                                                                                                                                                                                                                                                                                                          1885 TGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAATTTGCGAGCTGCTCAT 1944
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Pred. No. 22;
0; Mismatches
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OTHER INFORMATION: Clone ID: 701054355H1
US-09-878-574-11358
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                                                                                                                                                                                                        US-09-878-574-11381
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Best Local Similarity 52.6
Watches 90; Conservative
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APPLICANT: Byrum, Joseph R.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
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PRIOR FILING DATE: 1999-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Byrum, Joseph R. APPLICANT: La Rosa, Thomas APPLICANT: Thompson, Micha
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LOCATION: (1394)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             645 GTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTG 704
                                                                                                                                                                                                                                                                               132 TTGATAAGGAGAAGAAGGAGCTTGATGCAGAGGTTCATCGGAAATATGTTT 182
                                                                                                                                                                                                                                                                                                                 765 TCTTGGAGGAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTT 815
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                                                                                                                                                                                                                                                                                                                                                                                                                          12 GTGCTCTCCTTGATGTTGGTCTTATTAGGACTACAACCGGTAACCGTGTGTTTGGTGCCC 71
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79.0%;
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Pred. No. 0.065;
0; Mismatches
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; ORGANISM: Glycine max;
; OTHER INFORMATION: Clone ID: 701064379H1
US-09-878-574-11381
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1242
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LENGTH: 2526
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LENGTH: 263
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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Best Local Similarity
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PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24
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                                                                                                                                                           1271
                                                                              1331
                                                                                                                                                                                                                                          1211 TACTAGCAGATACAAACAACCAGCTCAAGATCAAGATTCAAGAACTTGAAGGATATCTGG
                                                                                                                                                                                                                                                                                 408 TTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGG 467
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                                                                                                                 TGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTG 587
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AAGCATCTGGAGTTGCTGATACT 1413
                                     AAGAAACAGGAATCTCTCATAGT 610
                                                                          TGATTACAAAGTTGAAATCCCATGAAAACGTAATCGAGGAGCACAAAAGGCAGGTTCTTG
                                                                                                                                                           ATTCTGAGAAGGAAACCGCAATCGAAAAGTTAAACCAGAAAGACACAGAAGCTAAAGACT 1330
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                                                                                                                                                                                                                                                                                                                                         Score 39.8;
Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.4; DB Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                          Mismatches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                     154 GAAGCGTATCAATGGTGAAATCATAAGCGGTGATTCTATGCAAGTTTACAAACATATGAA
                                                                                                       142 CCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGA 201
                               202 CATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAG 261
                                                                                                                                        214 TATTGTAGTAATTGTGGGGCCAACTGCTTCAGGTAAAACAGAGCTTAGCATAGAACTCGC 155
   94
                                                                                                                                                                        82 TCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGG 141
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Genomic DNA . SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 846 base pairs
TYPE: nucleic acid.
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
TATTGGAACTGCACAAGTAACACCTGAAGAAATGGATGGTATTCCACATCATTTAATTGA 35
                                                                                                                                                                                                                    109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Gimm1, Edward R
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/936,165 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: PA
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                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides,
Polypeptides and Their Uses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reichard, Richard
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51.7%;
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US-09-925-301-410
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SEQ ID NO 410
LENGTH: 140
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LENGTH: 2952
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APPLICANT: Rosen et al.
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                                                                                                                                                                                                                                                                                                                                       Sequence 410,
                                                                                                                                                                                                                                                                                                                 Sequence 410, Application US/09925301 Patent No. US20020052308A1
                                                                                                                             TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA106 CURRENT APPLICATION NUMBER: US/09/925,301 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08 PRIOR FILING DATE: 2000-03-08
                                                                                       PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 896 SOFTWARE: Patentin Ver. 2
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                                          SOFTWARE:
                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US00/05918 PRIOR FILING DATE: 2000-03-08
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CURRENT FILING DATE: 2001-08-10
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                                             PatentIn Ver.
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Pred. No. 0.096;
""smatches 71;
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Matches 160; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                         2245
                                                                                                                                                                                                                                                                               2425 TAGTTATTGTAGGACCCACTGCGGTGGGGAAAACAGCATTAAGTATTGCTTTAGCAAAAA 2366
                                                                                                                                                                                                2365 AATTTAATGGTGAAATTATTAGCGGTGACTCCATGCAAGTTTATCGCTCGTTAGACATTG 2306
                                                                                                                                                        207 TCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGCTTTG 266
                                                                                                                                                                                                                      147 GGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCCTAGACATCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/044,031
FILING DATE: 1997-05-06
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      87 TAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diske
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven Barash
TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles A. Kunsch
Patrick J. Dillon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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TTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTATTACA 386
                                       GTGAAGTCAGCGAAACATATT----CTGCCGCTGATTTTCAGAAAGAGGGGTCGTCAAAAAA
                                                                             TGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGA 326
                                                                                                                  LENGTH: 8519 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/070,927A FILING DATE: 04-May-2000
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SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (301)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                               2.5%;
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Pred. No. 0.0017;
D; Mismatches 161;
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US-08-781-986A-800/c : Sequence 800, Application US/08781986A : Publication No. US20030054436A1
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                             926
                                                                                                                                                            866
749
                                        384
                                                                                                                                                                                                                                                                                                                           986 AGCGTATCAATGGTGAAATCATAAGCGGTGACTCTATGCAAGTCTACAGACATATGAATA 927
                                                                                                                                                                                                                                                                                                                                                               144 AGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Ke
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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ATATTCAATCATTAATATAA 728
                                    ACATTGAATCTCTGCTCTGGAA 405
                                                                            TAATTACTGATATAACGAATAGAGGTAAAGTTCCAATCATAGCAGGTGGAACAGGCTTAT 750
                                                                                                     TGATTGAAGATATTTTGCCCGAGACAAAATTCCTATTGTTGTGGGGGGAACCAATTATT 383
                                                                                                                                                                                                  TTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTC 323
                                                                                                                                                                                                                                           TTGGAACTGCAAAAGTNACACCTGAAGAAATGGATGGTATTCCACATCATTTAATTGATA 867
                                                                                                                                                                                                                                                                                   TCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACGATGATCAGCT 263
                                                                                                                                                                                                                                                                                                                                                                                                 2.48;
cal Similarity 51.98;
136; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 123;
                                                                                                                                                            -CAGCATATGAATTCAAGCGATTAGCAGAAGATT 810
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OTHER INFORMATION: MAP TO AL033527.25

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.98

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2

OTHER INFORMATION: SWISSPROT HIT: BE242161.1, EVALUE 3.00e-72

OTHER INFORMATION: SWISSPROT HIT: Q9KAC3, EVALUE 2.00e-03
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 26692
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT: Chen, Wensheng
ITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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APPLICATION NUMBER: PCT/US01/00664
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Hanzel, David K.
           Conservative
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      Score 138; DB; Pred. No. 1e-
                           DB 10;
1e-30;
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                                               Length 138;
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2133
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn ver.
SEQ ID NO 2133
LENGTH: 903
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Best Local Sim:
Matches 175;
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URRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES 
LLE REFERENCE: 249-125
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                                                                                                                                                         185
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                                                                     245 CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC
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    ATTATTACATTGAATCTCTGCTC
                                                                                              CTGCTCTGATTGAAGATATATATTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCA
                                                                                                                                                                                                                                                                                                                                TAGCCCACAAGCTTGACGGTGAAGTAGTCAATGTGGATTCCATGCAGCTGTACAAAGGCA
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TATEISHI, NAOKO
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OZAKI, AKIO
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: Sequence 10050, Application US/09864761

: Patent No. US20020048763A1

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Best Local Similarity
Matches 318; Conserv
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SEQ ID NO 4310
LENGTH: 318
                                                                 APPLICANT:
                                                                            APPLICANT: Penn, Sharron G.
                                      APPLICANT:
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       OF INVENTION:
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28
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FILING DATE: 2000-03-17
APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
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T: Rank, David R.
T: Hanzel, David K.
T: Chen, Wensheng
T: Chen, Wensheng
INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-00-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
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Best Local S
Matches 145
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LENGTH: 457
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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SOFTWARE: Annomax Sequence
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OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BOLE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
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ORGANISM: Homo
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OR APPLICATION NUMBER: PCT/US01/00665

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00668

OR FILING DATE: 2001-01-30

OR APPLICATION NUMBER: PCT/US01/00663

OR APPLICATION NUMBER: PCT/US01/00663
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TCAGAAATAGAGCAACTGCTCTGAT 306
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Pred. No.
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RESULT 2
US-09-764-853-364

Sequence 364, Application US/09764853

Patent No. US20020090672A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
FILE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06

CURRENT APPLICATION NUMBER: US/09/764,853

CURRENT FILING DATE: 2001-01-17

CURRENT FILING DATE: 2001-01-17
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NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 364
LENGTH: 717
          NAME/KEY: SITE
LOCATION: (625)
OTHER INFORMATION: I
NAME/KEY: SITE
LOCATION: (655)
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NAME/KEY: SITE
LOCATION: (619)
OTHER INFORMATION: r
                                                                                                                    ORGANISM: Homo
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  INFORMATION:
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                                                                              Sequence 4310, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
          APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCI
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
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; NAME/KEY: SITE
; LOCATION: (673)
; OTHER INFORMATION: n
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n
US-09-764-853-364
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Best Local
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                                                                                  GCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTGAAGAAACAGGAAT
                                                                                                                            CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCAT
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Perfect score:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEM_PUB.seq:*
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2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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US-09-978-574-11368
US-09-878-574-11381
US-09-878-574-11381
US-09-938-842A-1242
US-09-938-935-232-642
US-09-935-323-300
US-09-955-302-310
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US-09-738-626-2133
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8702.120 Million cell updates/sec
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                                                                     Sequence 2133, Ap
Sequence 800, Appl
Sequence 800, Appl
Sequence 65, Appl
Sequence 261, Appl
Sequence 410, Appl
Sequence 11368, A
Sequence 11381, A
Sequence 1242, Ap
Sequence 5, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 310, App
Sequence 7419, Ap
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Sequence 364, App
Sequence 4310, Ap
Sequence 10050, A
Sequence 26692, A
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	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
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,	Sequence 2920, Ap	Sequence 1, Appli	Sequence 193, App	Sequence 316, App	Sequence 836, App	Sequence 712, App	Sequence 756, App	Sequence 202, App	Sequence 202, App	Sequence 199, App	Sequence 199, App	Sequence 580, App	Sequence 3, Appli	Sequence 21, Appl	Sequence 31, Appl	Sequence 1669, Ap	Sequence 1669, Ap	Sequence 1669, Ap	Sequence 1669, Ap	Sequence 187, App	Sequence 119, App	Sequence 36, Appl	Sequence 8765, Ap	Sequence 1074, Ap	Sequence 104, App	Sequence 11218, A

## ALIGNMENTS

RESULT 1 US-09-764-853-166

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                                                                                                                                   OTHER INFORMATION: n equals a,t,g, or US-09-764-853-166
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 166
LENGTH: 717
TYPE: DNA
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 166, Application US/09764853
Patent No. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
                                                                                                   Query Match
                                                                                                                                                                INAME/KEY: SITE
LOCATION: (655)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (673)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (713)
DIFFER INFORMATION: n e
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NAME/KEY: SITE
LOCATION: (625)
OTHER INFORMATION: n e
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LOCATION: (619)
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                 Local Similarity 98.4 es 685; Conservative
                              1 CTGCCATAAGATGGCGTCCGTGGCGGCTGCACGAGCAGTTCCTGTGGGCAGTGGGCTCAG
32.5%;
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Pred. No. 1.1e-185;
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; OTHER INFORMATION: Incyte ID No: hu01253362
US-09-532-315B-3471
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NUMBER OF SEQ ID NOS: 42212
SOFTWARE: PERL Program
SEQ ID NO 3471
LENGTH: 392
TYPE: DNA
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Best Local Similarity 99.5%;
Matches 387; Conservative
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PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR FILING DATE: 1993-08-03
PRIOR FILING DATE: 1998-01-16
PRIOR FILING DATE: 1998-01-16
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APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
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JRRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                PLICANT: Mullahy, Sara J.
PLICANT: Naughton, Rebecca E.
PLICANT: Naughton, Rebecca E.
PLICANT: Naughton, Rebecca E.
                                                  1981 TACAAATCTATATTTTTTTTTGAAGTTTAA 2009
                                                                                                                                            1861 CTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGA
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                                                                                                                          240 CTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/179,873
FILING DATE: 1994-01-11
APPLICATION NUMBER: 08/504,732
FILING DATE: 1995-07-20
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FILING DATE: 1995-05-10
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Search completed: April 21, 2003, 18:41:26 Job time ; 1168.24 secs

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APPLICANT: Scalinamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING OR REG
FILE REFERENCE: PD-1002 CIP
CURRENT FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 07/916,491
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR APPLICATION NUMBER: 09/008,119
                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-532-315B-3472
                                                                                                                                                                                                                                                                                  Sequence 3472, Application US/09532315B
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; OTHER INFORMATION: Incyte ID No: hu01286535
US-09-532-315B-3472
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NUMBER OF SEQ ID NOS: 42212
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LENGTH: 555
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OR FILING DATE: 1994-02-14
OR APPLICATION NUMBER: 08/282,991
OR FILING DATE: 1994-07-28
OR APPLICATION NUMBER: 08/438,571
OR FILING DATE: 1995-05-10
OR APPLICATION NUMBER: 08/179,873
OR FILING DATE: 1994-01-11
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Pred. No. 1.6e-132;
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RESULT 13
US-10-144-771-2119
; Sequence 2119, Application US/10144771
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SX:
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/10/144,771
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 2119
; LENGTH: 2103
; TYPE: DNA
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NUMBER OF SEQ ID I
SEO ID NO 2119
LENGTH: 2103
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Pred. No. 2.5e-267;
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US-60-453-050-276
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Best Local Similarity 98.1
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 276
LENGTH: 1271
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CURRENT APPLICATION
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-60-453-050-276
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98.1%;
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GENERAL INFORMATION:
GENERAL INFORMATION: Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF FILE REFERENCE: CL001380
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 41124
LENGTH: 1271
TYPE: DNA
ORGANISM: HUMAN
US-10-170-235-41124
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US-10-170-235-41124
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Best Local Similarity
Matches 1095; Conserv
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Conservative
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Pred. No. 2.1e
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US-60-453-135-276
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        APPLICANT: CARGILL, Michele
APPLICANT: LAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION.
FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 276
LENGTH: 1271
TYPE: DNA
TYPE: DNA
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ORGANISM: Homo
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CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-453-050-274
                                                                                                                                                                                               US-60-453-050-274
, Sequence 274, Application US/60453050
; GENERAL INFORMATION:
, APPLICANT: CARGILL, Michele
; APPLICANT: LUKE, May
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                                                                                                                                                                 TITLE OF INVENTION: GENETIC POLYMORPHISMS TITLE OF INVENTION: STENOSIS, METHODS OF FILE REFERENCE: CL001457
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                      Score 1353.8;
Pred. No. 0;
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AAAGCATTTTTTTTTTTTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGCACAGATTCC
                                TAACAAAGAACCTAAAGAGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAG
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RESULT 8
US-60-453-135-274
; Sequence 274, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
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                           CTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAAT
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Pred. No. 0;
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Db 1620
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Оу 2036
RESULT 7 US-10-170-
GENERA: APPLIO TITLE TITLE
FILE REFERENCE: CL001380 CURRENT APPLICATION NUMBER: US/10/170, CURRENT FILING DATE: 2003-03-17 NUMBER OF SEQ ID NOS: 42514 SEQ ID NO 41123 LENGTH: 1719 TYPE: DNA
Query Match Best Local Similari Matches 1456; Cons
Qy 568 Db 182
Qy 628
Оу 688
Qy 748
שמ 362
Qy 808
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48
QY 928
Db 542
Оу 939
Db 602
ОУ 970
Оу 1030

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GAGTTATTATCACTGCTGTCTTTCTATTGAGTTACAAATCTATATTTTATTGATGTTTA
                                                     GACTCTGGCTAAAATTATCTAATTTCCAGATGCTTTTGTAGATGACTGAAGTATTTGTGA 1768
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APPLICANT: Wan de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
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; ORGANISM: Homo sapiens
US-10-342-887-1692
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PRIOR ETILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1692
LENGTH: 1749
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Best Local Similarity
Matches 1660; Conserv
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Pred. No. 0;
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Sequence 275, Application US/60453050

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 2119
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nilarity 94.4%;
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Pred. No. 0;
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RESULT 4

US-60-453-135-275

US-60-453-135-275

Sequence 275, Application US/60453135

SEQUENCE 275, Application US/60453135

GENERAL INFORMATION:

APPLICANT: CARGILL, Michele

APPLICANT: LAKOUBOVA, Olga

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECT

FILE REFERENCE: CL001456

CURRENT APPLICATION NUMBER: US/60/453,135

CURRENT FILING DATE: 2003-03-10

NUMBER OF SEQ ID NOS: 82762

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 275

LENGTH: 2119

TYPE: DNA

ORGANISM: Homo sapiens
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94.4%; Pred. No. 0;
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	TGGCTGCCAAGCTGCATCACATGACAAACGCAAAAGTGGCCAGGAGCTTGCAAGTTTT	527	Qy
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4	GACAAAATTCCTATTGTTGGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAA	361	Дb
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US-10-170-235-40554

; Sequence 40554, Application US/10170235

; GENERAL INFORMATION:
   APPLICANT: VENTER, J. Craig

; TITLE OF INVENTION: KITS, SUCH AS NUCLEIC AC

; TITLE OF INVENTION: TRANSCRIPTS, FOR DETECT

; FILE REFERENCE: CL001380

; CURRENT APPLICATION NUMBER: US/10/170,235

; CURRENT FILING DATE: 2003-03-17
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LENGTH: 2119
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Best Local Similarity 94.7
Matches 2008; Conservative
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                                                                GTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTCTGCATAGCAGAAAAGCTCCCACCATTTT
                                                                                                  CACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGAAGAAGATTGGACTCAGAT
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PRIOR FILING DATE: 2000-09-11
INUMBER OF SEQ ID NOS: 888
SOFTWARE: Custom
SEQ ID NO 119
LENGTH: 2130
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (191)..(1426)
US-10-380-731-119
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Matches 2025; Conservative
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              TTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTTGGAGGAACTAAGAGATTTT 787
                                                                       AAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGC
                                                                                      AAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGC 727
                                                                                                    AGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTGGTCCCCTTGGAGGTCCTCTG 667
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                            CACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATC 847
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Qy	Qy Db	Дy	Оy	Qy Db	Qy Db	Qy Db	Ф	ОУ	Qy	Oy Db	Qy Db	Qу	Qy Db	Qy Db	Qy V	Db Qy	dg V	Db Db
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TTCTCGGAATTCTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTG	ATTTGAGTGAATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAG	ATTICCAGAIGCTTITGTAGAIGACTGAAGTATITGTGAGCCACATAIIGGGAGTTCTAG	GGATTGACTGCATCCCTTTAAAAGAAGTTTTATGTCCCTGACTCTGGCTAAAATTATCTA	TTAAAAGCAGCACAGATTCCACATTTTATACATGAGGATCTTCTTTGTGGTGAATACCA	TGGAAATGATGTAGTTCAGGAAAGCATTTTTTTTTTTTT	CTCACGTTCTCTATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTGTGGCTGATGTGTC	GCGGAATTCTCTGCATAGCAGAAAAGCTCCCACCATTTTCTTTTGATGTGGTTTTAAAGT	GGGATCCAGTTCAGGAGGGAGGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTAT	CAAGAGCTGAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTG 	CAGAGTGTTTCCCCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCAGGGCAGAAT	TTGAACCAACTGAAGAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGT 	TGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCAC 	CCAATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTC	CATCCAGGGCCACAAGCCTACAGCCACT                 CATCCAGGGCCACAAGCCTACAGCCACT	ATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTT	TATGCCCGGAAACAAAACCGATGGGTTAAAAACCGTTTTTGAGCAGACCTGGT	ANCCAGCTTCTAAAGAAAGGTATTGAGGCTCTGAAACAAGTAACTAAG	
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CURRENT FILING DATE: 2003-03-14 PRIOR APPLICATION NUMBER: 09/659,671	y 1130 TGTGATCGAATCATTGGGGATCGCGAATGGGCAGGCACATAAAAATCCAAATCCCAC 1189 	Qy
APPLICANT: Hyseq, Inc  APPLICANT: Hyseq, Inc  FILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  FILE REFERENCE: 21272-114  CHERENT APPLICATION UNMERS. HS/10/740.731	Y 1070 CCAATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTC 1129 	Qy Db
RESULT 2 US-10-380-731-119 Sequence 119, Application US/10380731 GENERAL INFORMATION	Y 1010 CTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGGCCACT 1069 	Qy Db
 AAAAAAAAAAAA	Y 950 ATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTT 1009 	Qy Db
2059	939GACCTGGTCCC 949	Qy Db
999	908 CTGGAGACTAGTAACCAGCTTCTAAAGAAAG938 	Qy Db
1939	### 848 TICCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACA 907	Qy Db
1879	788 CACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATC 847 	Qy db
1819	/ 728 TIGGATAAGAGGGIGGATGACATGCTTGCTGCTGGGCTCTTGGAGGGAACTAAGAGATTIT 787 	Qq dd
760	/ 668 AAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGC 727	Qy Db
1700	608 AGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTGGTCCCCTTGGAGGTCCTCTG 667	dg Vy
1640	7 548 CATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTGAAGAAACAGGAATCTCTCAT 607	Qy Db
1580	488 CTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCA 547	Qy Db
20	7 428 CAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGT 487	Оу
1460	368 GGAGGAA         380 GGAGGAA	Qу Db
1400	308 AATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTG 367 	Qy db
1340	7 248 CACCACATGATCAGCTTTGTGGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGA 307	Qy Db
TOPACCORCIO CONTROL DE CONTROL	188 TATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGG 247 	Qy Db
Db 1220 TGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCACATAAAATCC		Db

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AAAA 2041
                      AATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAG 1938
                                                                                                  AATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAG 1849
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Post-processing: Minimum Match 0%
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/cgn2_6/ptodata/2/pna,
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/cgn2_6/ptodata/2/pna/USC6_NEW_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
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                                      6 US-09-659-671A-134
B US-10-380-731-119
B US-10-170-235-40554
11 US-60-453-135-275
11 US-60-453-135-275
2 US-10-170-235-41123
2 US-10-170-235-41123
2 US-60-453-135-274
2 US-60-453-135-276
2 US-60-453-135-347
2 US-60-532-315B-347
2 US-09-532-315B-347
2 US-09-532-315B-3529
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Million cell updates/sec
Sequence 134, App
Sequence 119, App
Sequence 275, App
Sequence 275, App
Sequence 1692, Ap
Sequence 2113, Ap
Sequence 274, App
Sequence 274, App
Sequence 276, App
Sequence 276, App
Sequence 276, App
Sequence 3471, Ap
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Best Local Similarity
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Asundi, Vinod
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200.6	200.6	200.6	200.6	200.6	200.6	200.6	208.2	220.4	227.4	230	230	232	235.8	237.2	239	239.2	242.4	247	255	256	257.8	261.4
	•		٠	٠	9.8	•	•		11.1	11.3	11.3	11.4	11.6	11.6	11.7	11.7	11.9		12.5		12.6	12.8
201	201	201	201	201	201	201	288	498	254	236	235	255	246	266	240	287	245	247	255	256	263	292
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US-60-453-050-18357	US-60-453-050-18354	US-60-453-135-18368	·US-60-453-135-18364	US-60-453-135-18362	US-60-453-135-18357	US-60-453-135-18354	US-09-532-315B-7599	US-09-912-293-203132	US-09-532-315B-9516	US-09-532-315B-9525	US-09-532-315B-9513	US-09-532-315B-9520	US-10-349-781-40576	US-09-532-315B-9507	US-09-532-315B-9515	US-09-532-315B-9504	US-09-532-315B-9523	US-09-532-315B-9505	US-09-532-315B-9511	US-09-532-315B-9508	US-09-532-315B-9510	US-09-532-315B-9506
Sequence 18357, A	Sequence 18354, A	Sequence 18368, A	Sequence 18364, A	Sequence 18362, A	Sequence 18357, A	Sequence 18354, A	Sequence 7599, Ap	Sequence 203132,	Sequence 9516, Ap	`	Sequence 9513, Ap	Sequence 9520, Ap	Sequence 40576, A	Sequence 9507, Ap	Sequence 9515, Ap	Sequence 9504, Ap	Sequence 9523, Ap	Sequence 9505, Ap	`	Sequence 9508, Ap	Sequence 9510, Ap	Sequence 9506, Ap

Title:

9

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/659,671A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 475
SOFTWARE: pt.Ft.genes Version 2.0
SEQ ID NO 134
LENGTH: 2130
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (191)..(1426)
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                                                                                                                                                                                                      Matches 2025; Conservative
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FILE REFERENCE: 794
128 GCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTC 187
                                                                                                                                        8 AAGATGGCGTCCGTGGCGGCTGCACGAGCAGTTCCTGTGGGCAGTGGGCCTCAGGGGCCTG 67
                                      CAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTG 127
                                                                                                                         ACGATTCCGTCCGTGGCGGCTGCACGAGCAGTTCCCGTGGGCAGTGGGCTCAGGGGCCTG
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Zhao, Qing A.
Ren, Feiyan
Xue, Aidong J.
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Wang, Jian-Rui
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Pred. No. 0;
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Search completed: April 21, 2003, 17:14:09 Job time : 6044.18 secs

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GENERAL INFORMATION:
APPLICANT: Ma, X1ao-Jun; Dotson, Stanton B.: Monsanto
TITLE OF INVENTION: Tumor Associated Molecules (TAMS):
TITLE OF INVENTION: and prevention of cancer
FILE REFERENCE: 3214
CURRENT APPLICATION NUMBER: US/09/705,256A
CURRENT FILING DATE: 1999-05-11
PRIOR APPLICATION NUMBER: US 60/164,285
PRIOR FILING DATE: 1999-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 6006
LENGTH: 1223
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                               TTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTC 1458
                                                                                                                                                             ACCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGA 1338
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                                                 CCACCATTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCTCTATAATAGAAACAGCAGG
                                                                                                 TTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTC
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CURRENT FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 8259
SEQ ID NO 6006
LENGTH: 1223
TYPE: DNA
ORGANISM: Homo saplens
US-60-164-285-6006
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APPLICANT: Ma, Xiao-Jun
TITLE OF INVENTION: Tumor Associated Molecules; FILE REFERENCE: 3214
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            ATGGGCAGCGCACATAAAATCCCAAATCCCACTTGAACCAACTGAAGAAAAGAAGAAGAAGATT 1218
                                                            GAACAAGAGAAGTTATCACCTGTGTGAGCCTCTGTGATCGAATCATTGGGGATCGCGA 1158
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Similarity 98.6%;
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Pred. No. 1.26
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                            ; OTHER INFORMATION: n equals US-10-222-911-874
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CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/757,028
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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SEQ ID NO 874
LENGTH: 1183
TYPE: DNA
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  Query Match
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM001C1N
                                                                                          NAME/KEY: misc_feature
LOCATION: (1172)
OTHER_INFORMATION: n equals
                                                                                                                                                  ORGANISM: Homo sapiens
                                                      NAME/KEY: misc_feature LOCATION: (1177)
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Be Ma	st Local Similarity 98.6%; Pred. No. 1.4e-226; tches 1107; Conservative 1; Mismatches 14; Indels 1; Gaps 1;	
Qy	CAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCCTGTCTATGGCTTAGAGG	
Ф	15 TAAAAACCGTTTTTTGAGCAGACCTGGTCCCATTGTCCCCCCCTGTCTATGGCTTAGAGGT 74	
Qy	979 ATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAG 1038	
Db	75 ATCTGATGTCTCGAAGTGGGAAGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAG 134	
Qy	1039 TTTCATCCAGGGCCACAAGCCTACAGCCAATAAAAGATGCCAATACAATGAAGCTGA 1098	
Db	135 TTTCATCCAGGGCCACAGGCCTACAGCCACTCCAATAAAGATGCCATACAATGAAGCTGA 194	
Qγ	1099 GAACAAGAGAAGTTATCACCTGTGTGAGCCTCTGTGATCGAATCATCAGTGGGATCGCGA 1158	
망	195 GAACAAGAGATATCACCTGTGTGACCTCTGTGATCGAATCATCATCATTGGGGATCGCGA 254	
Qy .	1159 ATGGGCAGCGCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGAAAG	
Db	255 ATGGGCAGCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGAAGAAGATT 314	
οy	1219 GGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACTATAACAAAGA 1278	
рь	315 GGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACCATAACAAGA 374	
Qy	CCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAG	
ф	375 ACCTAAAGAGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGA 434	
Qy	1339 GACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTTCAGGAGGGAG	
DЪ	435 GACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTTCAGGAGGGAG	
Оy	1399 TTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTC 1458	
Db	TCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGC	
Qy	1459 CCACCATTTTCTTTTGATGTGGTTTTTAAAGTCTCTCACGTTCTCTATAATAGAAACAGCAGG 1518	
DЬ	555 CCACCATTITCTTTTGATGTGTTTTAAAGTCTCACGTTCTCTATAATAGAAACAGCAGG 614	
Qy	TGTCAGCTCCTTGTGTGGCTGATGTGTCTGGAAATGATGTAGTTCAGGAAAGCATT	
Db	615 TCTTGTCAGCTCCTTGTGTGGCTGATGTGTCTGGAAATGATGTAGTTCAGGAAAGCATTT 674	
Qy	1579 TTTTTTTCTTTGAACCTTAAAGGTTCTATTAAAAGCAGCACAGATTTCCACATTTTTA 1638	
Db	675 TTTTTTTCTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGCACAGATTCCACATTTTTA 734	
Qy	1639 TACATGAGGATCTTCTTTGTGGGGAATACCAGGATTGACTGCCTCTTTAAAAGAAGTT 1698	
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CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR EILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 874
LENGTH: 1183
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LOCATION: (1177)
OTHER INFORMATION:
US-09-757-028-874
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US-09-757-028-874
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Best Local Similarity
Matches 1107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
LOCATION: (1172)
OTHER INFORMATION: r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo
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RESULT 11 US-10-172-118-1692

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CURRENT APPLICATION NUMBER: US/10/172,118
CCURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1692
LENGTH: 1749
TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM_017646
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1692, Application US/101721.
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Wan 't Veer, Laura
APPLICANT: Van 't Veer, Marc
APPLICANT: Van 't Veer, Marc
APPLICANT: Van 't Jver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Pr
FILE REFERENCE: 9301-175-999
FILE REFERENCE: 9301-175-999
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Best Local Similarity
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RESULT 10 PCT-US02-18947-1692

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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_017646
; DATABASE ENTRY DATE: 2001-06-18
PCT-USO2-18947-1692
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TITLE OF INVENTION: Diagnosis and Progr
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18
CURRENT FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1692
LENGTH: 1749
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ER APPLICATION NUMBER: US 09/399,720
ER FILING DATE: 1999-09-21
ER APPLICATION NUMBER: US 09/404,284
ER FILING DATE: 1999-09-21
ER APPLICATION NUMBER:
ER ERILING DATE: 1999-12-16
ER OF SEQ ID NOS: 10451
                                                                                                                                                                    ER FILING DATE: 1999-03-18

ER APPLICATION NUMBER: US 09/293,972

ER FILING DATE: 1999-04-15

ER APPLICATION NUMBER: US 09/274,861

ER TING DATE: 1999-03-23

ER APPLICATION NUMBER: US 60/125,453

ER APPLICATION NUMBER: US 60/125,453

ER FILING DATE: 1999-03-19
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                                                                                                                       APPLICATION NUMBER: US 60/126,605
FILING DATE: 1999-03-26
APPLICATION NUMBER: US 09/306,350
                                                                                                                                                                                                                                                     FILING DATE: 1999-U3-Z3
APPLICATION NUMBER: US 09/271,490
ETITING DATE: 1999-03-18
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APPLICATION NUMBER: US 09/234,611
FILING DATE: 1999-01-22
APPLICATION NUMBER: US 09/240,371
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-12-23
APPLICATION NUMBER: US 09/235,076
                                                                                            FILING DATE: 1999-05-07
APPLICATION NUMBER: US 09/306,350
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APPLICATION NUMBER: US 09/277,227
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; OTHER INFORMATION: (1283); OTHER INFORMATION: similar to gi1419759 in ; OTHER INFORMATION: Run with FASTXY 3.3t00, US-09-471-275-2814
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                                             GACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCC
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2098
; OTHER INFORMATION: a
US-60-172-360-26034
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APPLICANT: Lal. Preeti
APPLICANT: Lal. Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the Identific
TITLE OF INVENTION: Polynucleotide Sequence
FILE REFERENCE: GX-0007 p
CURRENT APPLICATION NUMBER: US/60/172,360
CURRENT FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 29838
SOFTWARE: PERL Program
SEQ ID NO 26034
LENGTH: 2101
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US-60-172-360-26034
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ORGANISM: Homo sapiens
FEATURE:
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                     CTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACA
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	GTGGTGGA 300          GTGGTGGA 300	y 241 CTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGA 	Oy Db
	CAGAGAAT 240          CAGAGAAT 240	Y 181 GCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAAT	Qy db
	SACTCCAT 180         SACTCCAT 180	Y 121 CACGCTGGCGTTGCAGCTAGGGCAGCGGCTGAGCGCGGTGAGATCGTCAGCGCTGACTCCAT	Qy Db
	3GCAAATC 120         GCAAATC 120	y 61 GGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATC	Qy
	GGCTCAG 60           GGCTCAG 60	Y 1 CTGCCATAAGATGGCGTCCGTGGCGGCTGCACGAGCAGTTCCTGTGGGCAGTGGGCTCA	Qy Db
2;	h 2108; 79; Gaps	Query Match 94.2%; Score 1923.6; DB 40; Lengtl Best Local Similarity 96.1%; Pred. No. 0; Matches 2025; Conservative 0; Mismatches 4; Indels	
		ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No: 977391.15 S-10-133-013-165	us, ; ; ; ;
		SEQ ID NO 165 LENGTH: 2108 TYPE: DNA	
	•	PRIOR EFFLICATION NOMEER: 00/28/,00/ PRIOR FILING DATE: 2001-04-27 NUMBER OF SEQ ID NOS: 271 SOFTWARE: PERL Program	~ ~ ~ ~
		FILE REFERENCE: PA-0049 US CURRENT APPLICATION NUMBER: US/10/133,013 CURRENT FILING DATE: 2002-04-25 COURRENT FILING DATE: 2002-04-25	
		APPLICANT: Astromoff, Anna APPLICANT: Bandman, Ola APPLICANT: Cocks, Benjamin G. APPLICANT: Cocks, Benjamin G.	~ ~ ~ ~
		ESULT 6 S-10-133-013-165 Sequence 165, Application US/10133013 GENERAL INFORMATION:	RE US ;
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                                                                                                                                                                Sequence 150, Application US/10097340
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
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APPLICANT:
APPLICANT:
                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Nucleic Acid Molecule: TITLE OF INVENTION: Assessment, Prevention FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                                  Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                    Xumei ZHAO
Karen GLATT
                                                                                                                  Peter VEIBY
                                                                                                                          Ami SEN
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                                                                         Rosemarie SCHMANDT
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LENGTH: 2129
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PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PASTSEQ for Windows Version
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OR FILING DATE: 2001-09-26
OR PELICATION NUMBER: 60/276,026
OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 60/324,967
OR APPLICATION NUMBER: 60/324,967
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                                                                                    CTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATTTTGCCCGAGACAAATTCCTAT
    CTCTCATAGTGAATTTCTCCCATCGTCAACATACGGAAGAAGGTGGTGGTGGTCCCCTTGGAGG
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GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et
TITLE OF INVENTION: Nucleic Acid Molecules and
TITLE OF INVENTION: Assessment, Prevention, an
FILE REFERENCE: MRI-030PC
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OR APPLICATION NUMBER: 60/324,967
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OR APPLICATION NUMBER: 60/325,102
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; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FASTSED for Windows Version 4.
; SEQ ID NO 152
; SEQ ID NO 152
; LENGTH: 2129
; TYPE: DNA
; ORGANISM: Homo sapiens
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RESULT 3
US-10-097-340-152
Sequence 152, Application US/10097340
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: John MONAHAN
APPLICANT: Sebastian HOERSCH
APPLICANT: Subbangi KAMATKAR
APPLICANT: Subbangi KAMATKAR
APPLICANT: Shubhangi KOVATS
APPLICANT: Shubhangi KOVATS
APPLICANT: Shubhangi KOVATS
APPLICANT: Peter USIBY
APPLICANT: Michael MORRISEY
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Rosenarie SCHWANDT
APPLICANT: Karen LU
APPLICANT: Karen GLATT
TITLE OF INVENTION: NUCLEIC Acid Molecules and Proteins For The
TITLE OF INVENTION: ASSESSMENT, Prevention, and Therapy of OvaFILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT APPLICATION NUMBER: US/25,025
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-03-14
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The Identification Ovarian Cancer

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RESULT 2
PCT-US02-07826-152
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PRIOR FILING DATE: 2001-03-14
PRIOR PPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-27
PRIOR PPLICATION NUMBER: 60/326,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-03-14
PRIOR PPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PRIOR APPLICATION NUMBER: 60/325,502
PRIOR PRIOR PRIOR DATE: 2001-09-26
PRIOR PRIOR PRIOR DATE: 2001-09-19
NUMBER OF SEO ID NOS: 363
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-07826-152
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SEQ ID NO 152
LENGTH: 2129
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Best Local Similarity
Matches 2033; Conserv
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TITLE OF INVENTION: Nucleic Acid Molecules at
TITLE OF INVENTION: Assessment, Prevention,
FILE REFERENCE: MRI-030PC
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RESULT 1
US-09-513-151-3
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2041 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
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GENERAL INFORMATION:
APPLICANT: MCGILL UNIVERSITY
TITLE OF INVENTION: THE C. ELEGANS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: SWABEY OGILVY RENAULT
                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/CA98/00803
FILING DATE: 20-AUG-1998
PROOR APPLICATION DATA: APPLICATION NUMBER: CA 2,210,251
FILING DATE: 25-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ctt, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: 514 845-7126
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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SYSTEM: Windows
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19 US-09-919-002-314
10 US-09-399-32-314
10 US-09-399-32-316
10 US-09-764-853-166
19 US-10-072-326-166
19 US-10-072-326-364
10 US-09-764-853-364
10 US-09-764-853-364
10 US-09-764-902-494
10 US-09-783-315-3472
17 US-09-652-121-891
15 US-09-652-121-7656
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                                                                                   ATGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCC
                                                                                                                                                    TGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAA
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Maximum DB seq length: 2000000000
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2041
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/cgn2_6/ptcodata/1/pna/US094_COMB.seq:
/cgn2_6/ptcodata/1/pna/US095B_COMB.seq:
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/ptodata/1/pna/US084_COMB.seq:*
/ptodata/1/pna/US085_COMB.seq:*
/ntodata/1/pna/US085_COMB.seq:*
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/ptodata/1/pna/US081_COMB.seq:*
/ptodata/1/pna/US082_COMB.seq:*
/ptodata/1/pna/US082_COMB.seq:*
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/ptodata/1/pna/US07_COMB.seq:*
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8512.654 Million cell updates/sec
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/cgn2_6/ptodata/1/pna/US6015_COMB.seq:
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/cgn2_6/ptodata/1/pna/US60303_COMB.seq:
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/cgn2_6/ptodata/1/pna/US6003_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6004_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US6006_COMB.seq:*
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08_COMB.seq:*
09_COMB.seq:*
10_COMB.seq:*
11_COMB.seq:*
12_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Query Match Length DB IJ Description

Result No.

Score

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49.6	50.2	50.2	50.2	50.2	51.5	52.2	52.2	53.3	53.3	76.3	76.3	80.6	92.8	93.5	94.2	94.5	94.5	94.6	94.6	100.0
1039	1041	1041	1041	1041	2103	1223	1223	1183	1183	1749	1749	1858	2101	2109	2108	2129	2129	2129	2129	2041
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US-09-359-922-3465	US-09-898-888A-8140	US-09-898-888-8140	US-09-340-623-8140	US-09-205-070-8140	US-60-360-207-2119	US-60-164-285-6006	US-09-705-256A-6006	US-10-222-911-874	US-09-757-028-874	US-10-172-118-1692	PCT-US02-18947-1692	US-09-471-275-2814	US-60-172-360-26034	US-60-324-185-33690	US-10-133-013-165	US-10-097-340-150	PCT-US02-07826-150	US-10-097-340-152	PCT-US02-07826-152	US-09-513-151-3
Sequence 3465, Ap	Sequence 8140, Ap				Sequence 2119, Ap	Sequence 6006, Ap	Sequence 6006, Ap	Sequence 874, App	Sequence 874, App	Sequence 1692, Ap	Sequence 1692, Ap	Sequence 2814, Ap		Sequence 33690, A	Sequence 165, App	Sequence 150, App		:-	Sequence 152, App	Sequence 3, Appli

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                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon indicroarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                             Sequence 457 BP; 120 A; 102 C; 110 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID No 1507; 487pp; English.
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RESULT 14
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Matches 145; Conserv
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                        04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                  30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                               WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Human bone marrow expressed single exon
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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Pred. No. 1.4e-29;
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(MOLE-)

MOLECULAR DYNAMICS INC

Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cell:

for

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RESULT 15
AAI11574/c
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Best Local Similarity
Matches 145; Conserv
                                                                                                   04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0508408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                        Probe #1507
                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI11574 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 457 BP; 120 A; 102 C; 110 G; 125 T; 0 other;
                                                                                                                                                                                                        30-JAN-2001; 2001WO-US00670
                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                        Probe; human; microarray; gene expression;
                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT
2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic acid probes useful
zing gene expression in human bone marrow -
                                                           MOLECULAR DYNAMICS
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                              Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.1%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                     for gene
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                                                                                        2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                        expression
                             Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1523; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                              457
                                                           INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
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Pred. No. 1.4e-29;
                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                                                                                                                                                                                                                                                                                                                                                                        analysis in
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                             DR;
                                                                                                                                                                                                                                                                                                                                         cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                        human cervical cell sample
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RESULT 12
ABA53262/c
ID ABA532
XX ABA532
XX ABA532
XX Human
XX Human
XX Human
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XX Human
XX Homo s
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XX WO2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      derived from mRNA of human breast, and then measuring the label
bound to each probe of the microarray. The probes are useful for
verifying the expression of regions of genomic DNA predicted to
cencede proteins. They are useful for genomic DNA predicted to
cencede proteins. They are useful for genomic BNA predicted to
cencede proteins. They are useful for genomic breast disease. Gene
cexpression analysis is useful for assessing the toxicity of chemical
cexpression analysis is useful for assessing the toxicity of chemical
cexpression occlis. The microarray of this invention presents a far greater
diversity of probes for measuring gene expression, with far less bias
than expressed sequence tag microarrays. The method is suitable for
crapid production of functional information from genomic sequence. The
present sequence is a single exon nucleic acid probe of the invention.
Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
                                                                                                                                                                                                                                  01-FEB-2002
                                                                                                                                                                                                                                                                                                       ABA53262 standard;
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                                                                                       WO200157277-A2
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                    ABA53262
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                                                                                                                                                                                                                                                                                                                                                                                                           TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTCTATGAAGGCCTAGACATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 242
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                                                                                                                                                                                                                                                                                                                                                                                           TCAGAAATAGAGCAACTGCTCTGAT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 391
                                                                                                                                                                                               foetal
                                                                                                                                                          foetal liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1534; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP; 120 A; 102 C; 110 G; 125 T; 0 other;
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2000GB-0024263
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                                                                                                                                                                                                                                (first entry
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                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                          gene expression; single exon nucleic acid
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                                                                                                                                                                                                                                                                                                       457
                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 145; DB 22;
Pred. No. 1.4e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                             nucleic acid
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                                                                                                                                                                                           probe #1567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                          probe; ss.
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30-JAN-2001; 2001WO-US00669

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AAK01519/c
ID AAK01519 standard; DNA; 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                    30-JAN-2001;
                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                            WO200157275-A2
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human brain expressed single exon probe SEQ ID NO: 1510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK01519;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGAAATAGAGCAACTGCTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGAAATAGAGCAACTGCTCTGAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; SEQ
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                                                                                                                                                                                                                                                                                                                   cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0180312.
2000US-0207456.
2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO 1567; 639pp + sequence listing; English
                                                                                                       2001WO-US00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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; Pred. No. 1.4e-29;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                         schizophrenia;
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RESULT 10
ABL17248/c
ID
ABL17248;
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AC
ABL17248;
XX
AC
ABL17248;
XX
AC
ABL17248;
XX
Drosophila melanogaster general formation of the parameter of the paramete
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                                                                                                                                                                                                                                                                               Query Match 7.9%;
Best Local Similarity 52.4%;
Matches 438; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1016176-ABL30511), expressed DNA sequences (ABL101640-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 3217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genomic polynucleotide SEQ
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genes from Drosophila and
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                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                               GGGCCTGCAACGGACCCTACCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATC 120
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                                                                                                                             CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCAT 180
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                                                                                                                                                                                                                                                                               Score 160.8; DB 23; Pred. No. 2.6e-33; 0; Mismatches 377;
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                                                                                                                                                                  GGGTGGACCCCTTCGCTATCCACACATCGTTCTCCTTTGGTTGCGTTGCCAGCAGGATGT
                                                                                                                                                                                                                        TGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGT
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                                                                                                                                                                                                                                                                                                                                             CCGTATTCACCCCAACAACCGGCGCAAGATCATCCGGGCTATCGAAGTGTATCAGAGCAC
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 TACGTCGGGAGTTCTGCAGACGATTGGCTACAAGGAGTTTATTCCCTATCTGATCA 4311
                   TCAACATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCA 890
                                                                                                                                     TCTAAACGAGCGATTGGATTCCCGCGTAGATGGCATGCTGGCCCAAGGGCTGCTCCCTGA
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                                                                  ACTACGACAGTTTCACAATGCCCACCATGCTACCACTGT--
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RESULT 11
ABA42839/c
04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                  ABA42839 standard; DNA;
                                                                                                  disease;
                                                                                                                      Human breast cell single exon nucleic acid probe #1534
                                                                                                                                       01-FEB-2002
                                         30-JAN-2001;
                                                        09-AUG-2001
                                                                       WO200157271-A2
                                                                                                          Human;
                                                                                    sapiens
                                                                                                         microarray; single exon
                                                                                                   cancer;
                    2000US-0180312
2000US-0207456
                                          2001WO-US00662
                                                                                                                                       (first entry)
                                                                                                    88
                                                                                                          probe;
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expression; breast;

30-JUN-2000; 03-AUG-2000; 21-SEP-2000;

2000US-0608408. 2000US-0632366. 2000US-0234687.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer in a patient; ----- or the compound to inhibit prostate (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3210; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 (e) selecting a composition for inhibiting prostate cancer in a patien(f) assessing the prostate cell carcinogenic potential of a compound;(g) determining whether prostate cancer has metastasized in a patient;(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                        is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                               ATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAAT 1859
                          AAAA 2041
                                                                      ACTNTGAAATTTGCGAGCTGNTCATGTGNGAACTNTTATCACTGCTGTCTTTCTATTGAG
                                                                                                                                                                     TCTACAGAGAAGGAAGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAG
                                                                                                                                                                                                                             ACTTTGAAATTTGCGAGCTGCTCATGTGTGTGTTATTATCACTGCTGTCTTTTTGAG
AAAA
                                                     TTACCNAATCTAGTATTTTATTGAAGTTGTTATAGAAAAACTGAACAGCACCATCAAAC
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2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                                                                                       Conservative
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2000US-207454P.
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79.1%;
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Matches 205;
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18-JUL-2000;
13-DEC-2000;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                          Sequence 582
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous prostate cells and correlating with presence of prostate cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                (d) assessing the efficacy of a
in a patient;
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                                                                                                                                                                                                 patient;
121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6-MAR-2000;
                                                    61
                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                       detecting presence of prostate cancer, stage of prostate cancer
          TCTACAGAGAAGGAAGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAG
                                                                 ATGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAAT 1859
                                                    AAGGCGGGAATGGGCCATCTCCATTGAGATGATTAACTGAACCACACTCCTTCTCATAAT
TCTACACACAAGGAGGGAATGAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAG
                                                                                                                                                                                    also
                                                                                                                   Similarity
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70
                                                                                                                                                                                                                                                                                                                                                                                               Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
                                                                                                        Conservative
                                                                                                                                                                                   useful as a
                                                                                                                                                          BP; 201 A; 114 C; 111 G; 156 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                               9652; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          marker;
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                                                                                                                    84.7%;
                                                                                                                                  . 98;
                                                                                                                                                                                   pharmacodyanamic or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; carcinogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
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                                                                                                                 Score 162; DB 23;
Pred. No. 3.3e-34;
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                                                                                                      Mismatches
                                                                                                                                                                                                                                                                            therapy
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                                                                                                                                                                                  pharmacogenomic marker.
                                                                                                                                                                                                                                                                           inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmacodyanamic marker;
                                                                                                                               Length
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1744
                15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1684 CCTTTAAAAGAAGTTTTATGTCCCTGACTCTGGCTAAAATTATCTAATTTCCAGATGCTT 1743
                                                                                                                                                                                                                        Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy.
                                                                                                                                                                                                                                                                                           Human colon
                                                                                                                                                                                                                                                                                                                                                                                         AAA00911 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL616
                                                  14-MAY-1998;
                                                                                  13-MAY-1999;
                                                                                                                                              W09958675-A2
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                            oestrogen receptor-negative
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                                                                                                                                                                                                                                                                                           cancer
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98US-0085426.
98US-0085537.
98US-0085696.
98US-0105234.
                                                                                99WO-US10602
                                                                                                                                                                                                                                                                                      cell line polynucleotide sequence
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                                                                                                                                                                                                       cancer; lung cancer; ss
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RESULT 8
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AC ABV1
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                            Human prostate
                                                                                                                                                                                                                                                                                         1099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                            13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                     1039
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                                                                                                                       ABV19646 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 300 BP; 83 A; 69 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide library used to determine cancerous states of mammalian
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                                                                                                                                                                                                                                                                                                                                   TTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGATGCCATACAATGAAGCTGA 1098
                                                                                                                                                                                                                                                                                                                                                                                                              ATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAG 1038
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                                                          (first entry)
                              expression marker cDNA 19637.
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                                                                                                                       CDNA;
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Crkvenjakov R, Dickson M, Drmanac
Garcia V, Jones LW, Stache-Crain
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Randazzo F, 1
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Pred. No. 3.
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Pot D, Kassam A;
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Human; prostate cancer; cytostatic; carcinogen;

pharmacodyanamic marker;

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RESULT 6
ABL68710/c
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Matches
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AAS40785-AAS41684 represent cDNA sequences encoding for the novel human enzyme polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 717
 Kidney cancer
                                             ABL68710;
                                                                  ABL68710 standard;
                       15-MAY-2002
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                                                                                                                                     GGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGG
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                      (first entry)
 related
                                                                  DNA;
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gene sequence
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Pred. No. 5.6e
2; Mismatches
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les 7;
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27-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2000;
05-JUN-2000;
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22-SEP-2000
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                                                                                                            (AVAL-) AVALON PHARM
                                                                                                                          2000US-237278P.
2000US-237294P.
2000US-237295P.
2000US-237316P.
2000US-237425P.
2000US-237604P.
2000US-237604P.
2000US-237606P.
2000US-237608P.
2000US-244867P.
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The present invention describes a method (M1) for anti-neoplastic agent. The method involves exposir agent to be tested for anti-neoplastic activity, or

od (M1) for screening i lves exposing cells to activity, determining

for a a change chemical

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Claim

1; SEQ

ID 7047; 44pp; English.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene

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2002-188264/24.

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26-JUL-2000; 26-JUL-2000; 14-AUG-2000;

2000US-0220963. 2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213.

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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                          preventing, pulmonary, c diseases -
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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17 - NOV - 2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                     WPI; 2001-465566/50.
P-PSDB; AAU23398.
                                                                                                         Claim 4;
                                                                                                                                  Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                       17-NOV-2000;
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                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                  CA,
                                                                                                         SEQ
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2000US-0249245.

2000US-0249264.

2000US-0249265.

2000US-0249297.

2000US-0249299.

2000US-0249300.

2000US-0250160.

2000US-0250391.
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2000US-0249212.
2000US-0249213.
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2000US-0255918

2000US-0256719

2000US-0251479

2000US-0251865

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22-AUG-2000
23-AUG-2000
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30-AUG-2000
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01-SEP-2000
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22-SEP-2000
23-SEP-2000
23-SEP

2000US-0234997. 2000US-0234998. 2000US-0235484. 2000US-0235834.

The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),

2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

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Matches 685;
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                                                                                                                                                                                                                               The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID
                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medicondition
                                                                                                                                                                                                              Sequence 717 BP;
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                                                                                                                                 CTGCCATAAGATGGCGTCCGTGGGCGCTGCACGAGCAGTTCCTGTGGGCAGTGGGCTCAG
CTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGA
                 CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCAT
                                                                                                       GGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATC
                                                        CACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGTCGTCAGCGCTGACTCCAT
                                                                                            GGGCCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATC
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DB; ABB10476.
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28-JUN-2000;
30-JUN-2000;
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07-JUL-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; infilammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ss.
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14-AUG-
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17-MAR-2000;
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2000US-20467P
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2000US-21488P
2000US-21489P
2000US-21829P
2000US-229963P
2000US-22914P
2000US-22914P
2000US-22914P
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2000US-22914P
2000US-22956P
2000US-22956P
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2000US-229343P
2000US-23943P
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2000US-184664P.
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  Query Match
                                                             The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST; expressed sequence tag; gene; ss.
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                            Sequence
                                                                                                                                                                                                                         Claim 1; SEQ ID NO 119; 509pp; English.
                                                                                                                                                                                                                                                   An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                            WPI; 2002-292408/33.
P-PSDB; ABB97295.
                                                                                                                                                                                                                                                                                                                                     Xue AJ,
                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2001; 2001WO-US26015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human coding sequence SEQ ID NO: 119.
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Yang Y,
                            2130
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                           BP;
                         620 A; 439 C; 522 G; 549
                                                                                                                                                                                                                                                                                                                                   Zhou P, Asundi V, Zhang J, Wehrman T, Drmanac RT;
  94.18;
Score 1921.2;
                           T; 0 other;
DB 24; Length 2130
                                                                                                                                                                                                                                                                                                                                                 Zhao
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Best Local Similarity
Matches 2041; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2041 BP; 589 A; 421 C; 502 G; 529 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 8; 93pp; English
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                                                                                                                     CTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGA 300
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            CTCTCATAGTGAATTTCTCCCATCGTCAACATACGGAAGAAGGTGGTGGTGCCCCTTGGAGG 660
                                                                                                                                                                                                                GGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCT 540
                                                                                                                                                                                                                                                                                                          TGTTGTGGGAAGCAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATAC 420
                                                                                                                                                                                                                                                                                                                                                                         CTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGA 300
TCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGA
                                                          CTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 0;
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1860	TGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATT	1801	Qy
	TTTTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGA	1741	ф
	CTTTTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAA	1741	Qy
1740	TTTTATGTCCCTGACTCTGGCTAAAATTATCTAATTTCCAGAT	. 1681	Db
1740	TCCCTTTAAAAGAAGTTTTAT	1681	Qy
1680	ACAGATTCCACATTTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGATTGACTGC	1621 1621	Qy Db
Ö	AGTTCAGGAAAGCATTTTTTTTTTTTGAACCTTAAAAGGTTCTATTATTAAAAGCAG	56	Db
62	TAGTTCAGGAAAGCATTTTTTTTTTTTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGC	1561	. 0y
1560		50	Db
1560	ATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTGTGGCTGATGTGTCTGGAAATG	1501	Qγ
G		4	מם
1500	GCATAGCAGAAAAGCTCCCACCATTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCT	4	٥٧
4	CAGGAGGGAGGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTC	1381	₽ \$
ن -	AAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAAGGTGGTGGTGAAATCCAG	i tu	, Db
38	GAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTT	32	Qy
N	CCAGACTATAACAAAGAACCTAAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGC	1261	фd
2	CCCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCT	1261	Qy
1260	AAGAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTT	1201	Dp.
1260	AGAA	1201	Qy
20	CATCATTGGGGATCGCGAATGGGCACGCACATAAAATCCAAATCCCACTTGAACCAACT	. 4	D
1200	TAACOADTTCCCAATGCCCACATAAAATCCCACTTGAAACTTGAACTTGAACCTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACCAACTTGAACACTTGAACCAACTTGAACACTTGAACCAACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACTTGAACACACTTGAACACTTGAACACACTTGAACACTTGAACACTTGAACACTTAACACACTTGAACACACTTGAACACTTGAACACTTAACACACTTAACACACTTAACACACTTAACACACTTAACACACTTAACACACTTAACACACACTTAACACACACACTTAACACACACTTAACACACACACTTAACACACACACTTAACACACACACACACACTTAACACACACACACTTAACACACACACACACACACACACACACACACACACACACA	_	
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1140	CCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGTGATCGAA	08	0
0		02	Db 2
1080	CTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGA	N	0γ
1020	TGTCTATGCCTTAGAGGTATCTGAATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACC!GC 	961 961	Oy
60	TGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCC	0	Db
0	ATGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCC	901	у
900	CAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGG	841	Db
900	GGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGT		Qy
840	ACTATCAA	781	дb
840	GATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAAATAGCCAGGACTATCAAC	781	Qy
780	≱Ξ	721	ДЪ
780	gagcgcttggataagagggtggatgacatgcttgcttgct	721	Qy

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                   661.8
661.8
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                             AAX36073
ABN59708
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ABA06698
AAS41268
AAS41268
ABL68710
AAA00911
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                                                            Human homologue of Novel human coding Human cDNA SEQ ID Human cDNA SEQ ID CDNA encoding nove Kidney cancer rela
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Human colon cancer
Human prostate exp
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steria	ABAC	24	4528	2	. 7	4	
Listeria monocytog		24	918	•	7.	40	
Mycobacterium tuk		22	29	•	58.4	39	O
n spliced		24	60	•	6	8	
bidopsis		21	376	٠	61	37	
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. epidermidis	AAH54468	22	775	3.2		ω	
. epidermidis		22	90	3.2		4	
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cum codí		22	980	•		27	o
orynebacterium		22	σ	3.7	75	26	
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la melano		23	228	3.7	75.8	24	o
phila		23	S	3.7	5	23	ი
#14700		22	æ		w	22	o.
#1072		22	æ	•	138	21	a
bone m	AAK3999	22	138	6.8	138	20	o
brain e	AAK1426	22	œ	٠	138	19	c
foetal liv	ABA6585	22	138		138	18	a
breast	ABA4796	22	138	•	138	17	ဂ
#1548 used	AAI3286	22	57	7.1	145	16	a
#1507	AAI1157	22	7	7.1	145	15	c
bone m	AAK2696	22	57	7.1	. 145	14	c
brain e		22	7	7.1	145	13	ი
foetal liv	ABA5326	22	7	7.1	145	12	ი
eas		22		7.1		11	O
Drosophila melanoc		23	99	7.9	160.8	10	a

## ALIGNMENTS

Human homologue of gro-1, referred to as hgro-1.

15-JUL-1999 (first entry)

AAX36073;

AAX36073 standard; DNA; 2041

ВP

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RESULT 1
AAX36073
AAX 36073
AX AAX3
AX AAX3
AX Huma
AX Huma
AX Huma
AX Huma
AX Homc
AX Hom

Molecular identity of the gro-1 gene - useful for cancer diagnosis and/or prognosis, and where compounds affecting encoded proteins a.
                                                                                                                                                            WPI; 1999-190615/16
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hap-1 gene; cancer; aging; longevity; tumour formation;
                                                                                                                                                                                                                                                       Barnes T,
                                                                                                                                                                                                                                                                                                                                                       (UYMC-) UNIV MCGILL.
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Search completed: April 21, 2003, 15:52:47 Job time: 7858.89 secs

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SOURCE
ORGANISM
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                                                                                                      JOURNAL
                                                                                                                          TITLE
                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                           1984 AAATCTATATTTTATTGAAGTTAAATAAAGAAAAATTTACAAGAAA 2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1924 TGAAATTTGCGAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTTCTATTGAGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1744 TTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGGAGTTCTAGATTTGAGTGAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345;
                               Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 25, 2002 this sequence version replaced gi:21912638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7047 from Patent W00194629
AX336538
AX336538.1 GI:18127257
              Center: Wellcome Trust Sanger Institute
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 198772)
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Center code:
                                                                                                                     Direct Submission
                                                                                                                                           Sehra,H
                                                                                                                                                                                                                                                                  AL606906.18
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                                                                                                                                                                                                                                                                                                                    AL606906 198772 bp DNA: linear ROD Mouse DNA sequence from clone RP23-121J14 on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Young, P.E., Augustus, M., Carter, K.C., Horrigan, S., Soppet, D.R. and Weaver, Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
74 c 54 g 11
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98.9%;
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Pred. No. 1.6e-78;
0; Mismatches 4
                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Web site: http://www.sanger.ac.uk
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-121J14 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

FOR further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.

Location/Qualifiers

1. 198772

/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-121J14"
/

gg ; δÃ γ B Š Вb δÃ Matches Query Match 195862 TAGACGCTGTCAGTGCCACAGGAAGTCAAAGTAATTCCCCAGACTGTGACCCGGAACGCA 195922 1344 1224 CAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCAGACTATAACAAAGAACCTA 1283 1284 Local TCGAGGGGAATCCTCGGGGCAGAGCACAATCAAGAGCTGAAGGCCAGTGTTTGAGAGACATAT AAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACAT 1343 540; Similarity Conservative 13.4%;
68.7%; 0 Score 273.2; DB Pred. No. 8e-60; Mismatches 198; Indels 48; Gaps 1403 195981 195921 195861 10;

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196131

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196082

196041

TCCCACGCCTGGACTGAGGAATGCTGGGC-

AGAAGGCCCCAC

19608

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196040

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196130

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195982

TCCCA-GTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAGAAAAGCTCCCAC

5 B 5

1643 TGAGGATCTTCTTGTGGTGAATACCAGGATTGACTGCATCCCTTTAAAAGAAGTTTTAT 1702

TTTCTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGCACAGATTCCACATTTTTATACA 1642

TTTCTTTGAACCTTAAAGGTTTTATTTTAGAACGAGGCACAGATCGCACATTTTCTACTT 196246

1582

-- TCAGCTCCTTGTGTGCCTGTTGTGTCTGGTAATGATGTAGTTCAGAGTGGGATT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.9%; Score 366; DB 2; Length 239888; Best Local Similarity 59.8%; Pred. No. 4.3e-84; Matches 1040; Conservative 0; Mismatches 415; Indels 285; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227808 CAGGTCTATGAAGGGCTAGACATCATCACCAAGAAGAACTCTGCCCAAGAGC--AGAAAG 227865
                                                                                                                                                                                                                                                                    228191 ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227986 GTGGTGGGAGGAACCAATTATTATACTGAGTCTCTGCTCTGGAAAGTTCTAGTAACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227926 TTTAGGAACAGAGCAACTGCCCTGATTGAAGATATTTTTGCTTGAGACAAAATTCCCCATT 227985
228307 TGTTGGGGCTCTGAAATAAGTAACTAAGAGAAATGCTGGGAAACAGAACCGATGGGTTAA 228366
                                                                                                                                                                            228202 GAGCCCTTGGCTAAGAGAGTGGATGGCATGCTGGCTGGCACACTTGGAAGAGCTGAGA 228261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                  722 GAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGCGCCTCTTGGAGGAACTAAGA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 GTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACC 421
                                             842
                                                                                                            782 GATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACAT 841
                                                                                                                                                                                                                                                                                                           662 CCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGAT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 CATCCACATGACAAAGGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 GATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302 TTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 CAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATC 241
                                           GGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAA 901
                                                                                      GATTTCCACAGACGCTAAAATCTTAAGAACATTTCAGAAACTAG----
                                                                                                                                                                                                                                                                                                                                                                                            TCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGT 661
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106138
120672
120772
137018
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166123
186223
213752
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/db_xref="taxon:10116"
/clone="CH230-172N14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106137: gap of unknown length
120671: contig of 14534 bp in length
120771: gap of unknown length
137017: contig of 16246 bp in length
137117: gap of unknown length
161673: contig of 24556 bp in length
161773: gap of unknown length
186122: contig of 24349 bp in length
186222: gap of unknown length
186222: gap of unknown length
213751: contig of 27529 bp in length
213851: gap of unknown length
213881: contig of 26037 bp in length
23881: contig of 26037 bp in length
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106037: contig of 11868 bp in
106137: gap of unknown length
120671: contig of 14534 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qualifiers
                                                                                                                                                                                                                                                                  -----CAGTTCTGGAT 228201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                      ----- 228306
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1920 229263	CTACAGAGAAGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGA	1861 229207	д Q
1860 229206	TGGCAGGAAAGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATT	1801 229154	DP 03
1800 229153	CTTTTGTAGATGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAA	1741 229094	Db Qy
1740 229093	ATCCCTTTAAAAGAAGTTTTATGTCCCTGACTCTGGCTAAAATTATCTAATTTCCAGATG	1681 229034	ДУ
1680 229033	ACAGATTCCACATTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGGATTGACTGC	1621 228986	Db Qy
1620 228985	TAGTTCAGGAAAGCATTTTTTTTTTTTGAACCTTAAAGGTTCTATTATTAAAAGCAGC	1561 228927	Фр
1560 228926	TATAATAGAAACAGCAGGTCTTGTCAGCTCCTTGTGTGGGCTGATGTGTCTGGGAAATGATG	1501 228867	DP QV
1500 228866	TGCATAGCAGAAAAGCTCCCACCATTTTCTTTTGATGTGGTTTTAAAGTCTCACGTTCTC	1441 228842	DB 02
1440 228841	AGGAGGGAGGGTATGTTTGTCTCCCA-GTCTGGGCAAAGGAGTGCTATGCGGAATTCTC	1382 228782	B 8
1381 228781	AAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTTC	1322 228731	D 02
1321 228730	CCAGACTATAACAAAGAACCTAAAGGGAAGGATCCCCAGGGCAGAATGATCAAGAGCTG	1262 228679	Dp QQ
1261 228678	AAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCC	1202 228633	Db Qy
1201 228632	ATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAACCAACTG	1142 228605	dd Vy
1141 228604	CCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGAACCTCTGTGATCGAATC	1082 228547	Qy Db
1081 228546	CTTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCCATAAAGATG	1022 228487	D Qy
1021 228486	GTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCT	962 228427	Оy
961 228426	TGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCCT	902 228367	DP QV

RESULT 14 AX336538/c LOCUS

AX336538

355 bp

DNA

linear

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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Coveeland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, K.J., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Edils, T., Ferraguto, D., Flagg, M., Ford, J., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Holloway, C., Hamilton, K., Falls, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, J., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Karlsson, E., Kelly, S., Khan, U., Leut, S., Liu, W., Joudes, H., Lozado, R.J., Lucier, A., Lucier, R., Luna, R., Ma, J., Kartinez, E., Massey, E., McLead, M., Landry, N., Leut, S., Liu, W., Loulseged, H., Lozado, R.J., Lucier, R., Martin, R., Martinez, E., Maheshwari, M., Mapua, P., Martin, R., Martinez, E., McLead, M., Martinez, E., McL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ***, 35 unordered pieces AC093939
                                                                                                                                                                                                                                                                                                                         Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Jul 10, 2002 this sequence version replaced gi:20335375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 239888)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Blanage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Burd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (12-SEP-2001) Human Genome Sequencing Center, Depar
of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 239888)
                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 239888)
Center project name: GEXQ
Center clone name: CH230-172N14
                                                                                                                                                                                                                    Center code: BCM
                                                                                                                                                                                                                                                       Center: Baylor
                                                                                                                                                                                                                                                                                                   ---- Genome Center
                                                                                                                                                                                                                                                   College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department
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COMMENT

TITLE

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as
                                                                                                                                                                                                                                                                                                                                        Chemistry: Dye-terminator Big Dye: 100% c Assembly program: Phrap; version 0.990325 Consensus quality: 210507 bases at least Consensus quality: 213691 bases at least Consensus quality: 215787 bases at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid;
   it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.990329
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Q30
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56933 63190 63290 68851 68951 76142 76242 76242 83348 48448 52408 52508 39841 42403 42503 7219 8600 8700 9999 10099 24919 29104 11308 12833 12933 15682 15782 18003 56833 48348 34816 34716 24819 1884 68850: 68950: 48347 gap conti gap o gap o gap gap o gap or conti gap o gap o gap o gap o gap of contig gap o gap o conti cont: f unknown leng y of 7006 bp 1 f unknown leng y of 10722 bp unknown
of 6257
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of 5845 e unknown g of 1525 unknown of 2749 unknown unknown f unknown
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Query Match
Best Local Similarity
Matches 1040; Conserv
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80065 TGTTGGGGCTCTGAAATAAGTAACTAAGAGAAATGCTGGGAAACAGAACCGATGGGTTAA 80124
                                                                                                79960 GAGCCCTTGGCTAAGAGAGTGGATGGCATGCTGGCTGGCACACTTGGAAGAGCTGAGA 80019
                                                                                                                                                                                                                                                                          542
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                       842 GGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGAAAA 901
                                                                                                                                                                       662 CCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGAT 721
                                              GATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACAT 841
                                                                                                               GAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGGCTCTTGGAGGAACTAAGA 781
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80851	92 ATCCTTTAAAAGAGAGTTCTTGTCCCTGGCGCTGGCTAAAAGTAATCTCATTTCCAG	807	뫄
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80791	44 ACAGGTTGCACATTCTTTCTTTTAGTGGTGAATACCAAGATTCAGTA	807	뫄
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80743	361 TAGTICAGGAAAGCATHTITTITTTTTTTGAACCITAAAAGGTTCTAITATTAAAAGCAGG 	908	B 5
606	25 TCTGCAGTGGAAACGCAGGTCTTTCAGCCCTTTGTGTGTG	6	, B
560	01 TATAATAGAAACAGCAGGT	15	Qy
80624	00 CGCCATCTTTCATTCTC	908	ДD
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80599		805	뭣
1440	82 AGGAGGGAGGGTATGTTTGTCTCCCA-GTCTGGGCAAAGGAGTGCTATGCGGAAT	13	Qy
80539	89 AAGGCCAGTGTTTGAGAGACATGCCTTTGCAGAGATGTGGGGATCAAG	4	8
1381	22 AAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGAT	13	Qy
1321 80488	262 CCAGACTATAACAAAGAACCTAAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTG	12	Db Qq
80436	91ATTGGACTTAGACGTGTCAGTGCCTAGGAAGCCAAAGTAATT	803	Db
1261	02 AAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGT	12	Qy
80390		803	Дb
1201	42 ATCATTGGGGATCGC	11	Qy
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80244	85 CCCCAACTCCCGCGCGTTATTGATGTTTCCAAGTGGGAGGAGTCTGTTCTGGAACCTGC		Db .
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AUTHORS
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Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M.,
Miner, G., Miner, E., Mtchell, T., Mohabbat, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
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Wu, C., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 181838)
Worley, K.C.
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Direct Submission
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                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be presented to the sequence as soon as it is available and the accession number will
                                                                                                                                                               be preserved
                                                                                                                                                                                                                                                                                           Sequencing vector: M13; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 115969 bases at least Q40 Consensus quality: 122034 bases at least Q30 Consensus quality: 127422 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
GGGTATGTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAG
                                                                                                                                                                                                                                                                     AGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACTAT 1270
                                                                                                                                                                                                                                                                                                                GATTTTGTCTTATCAGCGCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAGA 26095
                                                                                                                            AACAAAGAACCTAAAGAGAAGGGATCCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGC
                                                                                                                                                                                                                       AACAAAGAACCTAAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCAGC
                                                                                                                                                                                                                                                     AGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCCAGACCAT
                                                                                                                                                                                                                                                                                                                                                                               868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            53282
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:01170" 183512. .199863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93582. .101614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:01187
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45284 . . 4958:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:01823
fragment_chain:1"
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2379. .22743
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment:01894"
45915 c 45981 g 53154 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:00867
fragment_chain:4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:01960
fragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:01156
fragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_fragment:00339
fragment_chain:3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment:00292
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:01809
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment:00307"
155993. .167875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:01896
fragment_chain:4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tragment_chain:
101715. .107836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:00999
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:01177
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="assembly_fragment:00528"
                                                                                                                                                                                                                                                                                                                                                                                            41.18;
98.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .155892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .9348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .183411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .144546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 8655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .72764
                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                           Score 839.4; DB 2; Pred. No. 5.1e-208;
                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1531 others
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Length 199863;
                                                                                                                                                                                                                                                                                                                                                                              <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                           1450
                                                                                                                          25915
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                                                                                                                                                                                        25975
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REFERENCE
AUTHORS
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AC106650
LOCUS
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ORGANISM
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25495
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                                                                                                                                                                                                                                 Allen,C.,

Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,

Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,

Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,

Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,

Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chaves,D.,

Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,

Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,

Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,

Douthwalte,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,

Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,

Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,

Garrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,

Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,

Hernandez,O., Hodgson,A., Hodges,M., Holloway,C., Hollins,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGCAGGTCTTGTCAGCTCCTTGTGTGTGGGCTGATGTGTCTGGAAATGATGTAGTTCAGGA 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATTTTATTGAAGTTTAAATAAAGAAAAAATTTACAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATTTTTATTGAAGTTTAAATAAAGAAAAATTTACAAGA 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGCGAGCTGCTCATGTGTGAGTTATTATCACTGCTGTCTTTCTATTGAGTTACAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCAGAATTCTACAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCGGAATTCTACAGAGA 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA-TTTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGGATTGACTGCATCCCTTTA
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AC106650.2
HTG; HTGS_P
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Li, J., Liu, W., Louls Li, Liu, W., Louls Liu, W., Louls Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                        Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Johnson, R., Landson, R., La
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                           199863 bp DNA 1
Homo sapiens chromosome 1 clone RP11-473P22,
PROGRESS ***, 16 unordered nienna
                                                                                                                                 AL354888.6 GI:9863692
Direct Submission
                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                 Homo sapiens
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                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 198363; sum-of-contigs
Insert size: 201159; 6.2% error; agarose-fp
Quality coverage: 3.87x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
On Aug 21, 2000 this sequence version replaced g1:9213379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgesh CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: bA473P22
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Contact: humquery@sanger.ac.uk
----- Project Informa
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58359 64082; contig of 5724 bp in length
64083 64182; gap of 100 bp
64183 72764; contig of 8582 bp in length
72765 72864; gap of 100 bp
72865 86552; contig of 1368 bp in length
86553 86552; gap of 100 bp
86553 93481; contig of 6829 bp in length
93582 93581; gap of 100 bp
93582 101614; contig of 8033 bp in length
101615 101714 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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2279 2378: gap of 100 bp
2379 22743: contig of 20365 bp in length
2379 22744 22843; gap of 100 bp
22844 45183: contig of 22340 bp in length
45184 45233: gap of 100 bp
45284 45233: gap of 100 bp
45284 4581: contig of 4298 bp in length
49682 58258: contig of 8577 bp in length
58259 58358: gap of 100 bp
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155993 167875: conti
167876 167975: gap of
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                                                                                                        /db_xref="taxon:9606"
/chromosome="1"
              /note="assembly_fragment:00765
fragment_chain:1
                                                                            /clone="RP11-473P22"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk
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107836: contig of 6122 bp
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7649:

; contig c ; gap of 8977: cc

9: gap of 100 bp 8977: contig of 1328 bp in 7: gap of 100 bp 10103: contig of 1226 bp in

03: gap of 100 bp 11362: contig of 1159 bp in length

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12921: 11462: 10203: 9077:

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2: gap of 100 pp 2821: contig of 1359

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con : gap of 15283:

ap of 100 bp contig of 1176 bp in length

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7804:

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Best Local S
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1151 GATCGCGAATGGGCAGCACATAAAATCCCAAATCCCACTTGAACCAACTGAAGAAAAGA 1210
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                        Score 850.4; DB 2;
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0; Mismatches 11;
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con ; gap of 33818; corr 19 33918; dr

p of 100 bp contig of 1662 bp in

30317:

17: gap of 100 bp 32056: contig of 1739 l

ni dq

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100 bp 100 bp in '

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contig of

1250 bp in 1138 bp in

length

38379: contig of 1567 b

bp in

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con. . : gap of 40190:

p of 100 bp contig of 1711 bp in

bp in

35256: gap of 100 bp 36712: contig of 1456 bp

18: gap of 100 bp 35156: contig of 1238 bp in

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27373: 4 27473: GAT

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26235:

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24613:

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100 bp f 1522 t 100 bp f 1222 k

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23291:

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gap of 10.76: contig of 10.84: contig of

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contig of 1717 b

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49423:

1002: gap of 100 b 49323: contig of 1921 23: gap of 100 b

length

Gaps

47402:

46921:

100 bp 47302: contig of 381 b 174: gap of 100 bp 46821: contig of 1247 l 53: gap of 100 b 45474: contig of 1321 180: gap of 100 bp 44053: contig of 2173 bp in 100 bp 41780: contig of 1490 b

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44153:

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                                                                                                                                                                                                                                                                             CATTTTTATACATGAGGATCTTCTTTGTGGTGAATACCAGGATTGACTGCATCCCTTTAA 1690
                                                                                                                                                                                                                                                                                                                                 GGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTATGCGGAATTCTCTGCATAGCAG
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GGAGGGAATCAGACTGAGGAAGCTGTGACATAGGACTTGAAGACCAAAGACTTTGAAATT 1930
                                  GGGCCATCTCCATTGAGATGATTAAGTGAACCAAACTAGTTCTCAGAATTCTACAGAGAA
                                                                                                         TGACTGAAGTATTTGTGAGCCACATATTGGGAGTTCTAGATTTGAGTGAATGGCAGGAAA
                                                                                                                                                                                   AAGAAGTTTTATGTCCCTGACTCTGGCTAAAATTATCTAATTTCCAGATGCTTTTGTAGA 8186
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/note="L2 repeat: matches 2244.
32752. .33074
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/note="L2 repe
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33075, .33487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 14, 2000 this sequence version replaced gi:7770499. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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PROGRESS ***, 81 unordered rianna
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L.,
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                                                  NOTE: This is a 'working draft' sequence. It currently consists of 81 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                 Center project name: L7675
Center clone name: 204_L_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                ----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chrl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: proteins: Sw:P22004 Sw:P20722 Sw:P22003
Sw:P18075 Tr:Q9YGH7 Sw:P23359 Sw:P55105 Sw:P49003
Sw:P34820 Sw:P34821"
                                                                                                                                                                                                                                                                                                                                                                                                      /note="FLAM_C repeat: matches 1.
complement(4214. .4420)
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/note="match: cDNAs: Em:S77477 Em:X51801 Em:M97017 Em:UJ9545 Em:J04566 Em:X80992 Em:M60316 Em:M60315 Em:M97016 Em:X56906 Em:AF100787 Em:U40034"
                                                                                                                                                                                                                                                                                                                                           complement(4252. .4438)
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/gene="BMP8"
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5153. .5347,14838. .14986,15379. .15568,28682.
/gene="BMP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(830. .29381)
/gene="BMP8"
                                                                                                                                                    /note="MIR repeat: matches 57. .146 of consensus"
complement(8369. .8876)
                                                                                                                                                                                                                                     972. .6029
/note="MIR_repeat: matches 19. .75 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NMVVKACGCH
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NELPQANRLPGIFDDVHGSHGRQVCRRHELYVSFQDLGWLDWVIAPQGYSAYYCEGEC
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(osteogenic protein 2))"
(protein_id="cAB75681.1"
/db_xref="G1:7018292"
                                                                                                                                                                                                                                                                                                                                                             'note="match: STS: Em:T63436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ′translation-"mTALPGPLWLLGLALCALGGGGPGLRPPPGCPQRRLGARERRDV
?REILAVLGLPGRPRPRAPPAASRLPASAPLFMLDLYHAMAGDDDEDGAPAERRLGRA
>LVMSFVNMVERDRALGHQEPHWKEFRFDLTQIPAGEAVTAAEFRIYKVPSIHLLNRT
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/db_xref="taxon:9606"
/chromosome="1"
                                                                 note="AluJb repeat: matches 1.
                                                                                                          note="match: GSS: Em:B51067"
                                                                                                                                  'gene="BMP8'
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                                                                                                                                                                                                                                                                                                                        gene="BMP8
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clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMFQVVQEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRHKDLGLRL
      :e="AluJb repeat: matches 1.
75. .10242
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                                                                                                                                                                                                                                                                                                e="match: STS: Em:AA634039"
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                        .312 of consensus'
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.15568,28682. .29015))
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  'note="MIR repeat: matches 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="match:
                                                                                                                                                                                                                                note="MIR repeat: matches 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MIR repeat: matches 22. 1140. .21425
                                                                                                                                             note-"CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="L2 repeat: matches 2129.
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                                                                                                                                                                                                                                                                          ote="MIR repeat: matches 81.
                                                                                                                                                                                                                                                                                                                 ote="MIR repeat: matches 80.
                                                                                                                                                                                                                                                                                                                                                           note="AluSp repeat: matches 143.
                                                                                                                                                                                                                                                                                                                                                                                   note="L2 repeat: matches 2606. .2750 of consensus"
5215. .26275
                                                                                                                                                                                                                                                                                                                                                                                                                            note="MIR repeat: matches 50.
5018. .25159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 51.
3600. .23742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ote="AluJo repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ote="MIR repeat: matches 5. .71 of consensus" 1952. .22989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L2 repeat: matches 2361.
                                                                                                                                                                                             ote="L2
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RESULT 9 HS118J21/c LOCUS DEFINITION ACCESSION

VERSION KEYWORDS SOURCE ORGANISM CpG Islar AL033527 HALIBUZI

166496 bp DNA linear PRI 18-FEB-2000 Human DNA sequence from clone RPI-118J21 on chromosome lp34.1-35.3 Contains part of the gene for BMP8 (bone morphogenetic protein 8 (osteogenic protein 2)), an l-myc-proto-oncogene, STSs, GSSs and CDG Islands.n, complete sequence. Homo sapiens Homo sapiens. AL033527.26 GI:6456853

Sqo

Island; 1-myc; morphogenetic; oncogene; osteogenic

REFERENCE TITLE JOURNAL AUTHORS

Ellington, A.

(bases 1 to 166496)

Eukaryota;

Eutheria; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Mammalia;

COMMENT

Submitted (18-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone Submission

requests: clonerequest@sanger.ac.uk

On Nov 21, 1999 this sequence version replaced g1:6002299.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is amblguous, there is an annotation using the 'unsure'

feature key.

http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-118J21 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see The following abbreviations are used to associate primary accession numbers given in the feature table rath their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREWHBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at RP1-118J21 is Park Cancer

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      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                            Direct Submission
Direct Submission
Submitted (19-DEC-2001) National Institutes of
Gene Collection (MCC), Cancer Genomics Office,
Institute, 31 Center Drive, Room 11A03, Bethesd
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IMAGE:5042856, mRNA, col
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Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/ILNL at: Series: IRAK Plate: 41 Row: 1 Column: 20. Location/Qualifiers
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Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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Score 1119.4; DB 10;
Pred. No. 1.1e-281;
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S., Martin,
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                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1308)
Lemieux, J., Lakowski, B., Webb, A., Meng, Y., Ubach, A., Barnes, T. and Hekimi, S.
Regulation of physiological rates in Caenorhabditis tRNA-modifying enzyme in the mitochondria Genetics 159 (1), 147-157 (2001)
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Homo sapiens tRNA isopentenyl
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AY052768.1 GI:16209578
Lemieux, J.,
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            (bases 1 to 1308)
Barnes, T.
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            CATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATC
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Submitted (28-AUG-2001) Biology,
Pentfield Avenue, Montreal, QC H3
Location/Qualifiers
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 701991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone MGC:17002
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1 (bases 1 to 1844)
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Contact: MGC help desk
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                 /protein_id="AAH10741.1"
/db_xref="GI:14789611"
/translation="MGTEKVDIRKVELEKEDGLVLHKRLSQVDPEMAAKLHPHDKRKV
ARSLQVFEETGISHSEFLHRQHTEEGGGPLGGPLKFSNPCILMLHADQADERLDKRVD
DMLAAGLLEELRDFHBRYNQKNVSENSQDYQHGIFQSIGFKEFHEYLITEGKCTLETS
NQLLKKGIEALKQVTKRYARKQNRWVKNRFLSRPGPIVPPVYGLEVSDVSKWEESVLE
                                                                                                                    transferase"
                                                                                                                                                                     /note-"Vector:
166. .1140
                                                                                                                                                                                                     /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:17002 IMAGE:3905836"
   PALEIVQSFIQGHKPTATPIKMPYNEAENKRSYHLCDLCDRIIIGDREWAAHIKSKSH
                                                                                                                                    /product="Similar to
                                                                                                                                                     /codon_start-1
                                                                                                                                                                                                                                                                                                                         e following selection criteria: matched
Location/Qualifiers
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lsopentenylpyrophosphate transferase,
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AGAATGATCAAGAGCTGAAATGCAGCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGG
                                         AAAGTCAGAGTGTTTCCCCCAGACTATAACAAAGAACCTAAAGGGAAGGGATCCCCCAGGGC
                                                                                                   CCCACTTGAACCAACTGAAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAG
                                                                                                                                                              ACCTCTGTGATCGAATCATTGGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAAT
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             CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA
                                                                                                                                                                ATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-e 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Shibahara,T., Tanaka,T. and Nakamura,Y.
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Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL01371.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="COL01371"
/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector: p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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ARSLQVFEETGISHSEELHRQHTEEGGGPLGGPLKFSNPCILMLHADQAVLDERLDKR
VDDMLAAGLLEELRDFHRRVNOKNVSENSQDVQHGFSSIGFKEFHEYLITEGKCTLE
TSNQLLKKGIEALKQVTKRYARKQNRWVKNRFLSRPGPIVPPVYGLEVSDVSKWEESV
LEPALEIVQSFIQGHKCTATPIKMPYNBAENKRSYHLCDLCDRIIGDREWAAHIKSK
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1749 bp mRNA linear PRI 15-FEB-2002 cDNA FLJ23642 fis, clone COL01371, highly similar to tRNA isopentenylpyrophosphate transferase precursor

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E 2 (Bases I to 1749)

E 2 (Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,

Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission

AL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,

University of Tokyo, Deptment of Virology: Shirokane-dai, 4-6-1,

Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp,

Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of

International Trade and Industry of Japan; cDNA full insert

sequencing: Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing: Departent of

Virology and Human Genome Center, Institute of Medical Science,

Trivarsity of Tokyo (partly supported by Science and Technology
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Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
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/tissue_type="colon"
/clone_lib="COL"
/note="cloning vector
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                                                /organism="Homo sapiens"
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/clone="COL01383"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2216)
Golovko,A., Hjalm,G., Sitbon,F. and Nicander,B.
Cloning of a human tRNA isopentenyl transferase
Gene 258 (1-2), 85-93 (2000)
                                                                 2 (bases 1 to 2216)
Golovko,A. and Hjalm,G.
Direct Submission
Submitted (28-JUN-1998) Dep. of Plant Biology,
of Agricultural Sciences, Box 7080, SE-750 07 t
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                                   AATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCCGAGACAAAATTCCTATTGTTGTG
                                               AATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTTGTG
                                                                                   CACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGA
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FLSRPGPIVPPVYGLEVSDVSKWEESYLEPALEIVQSFIQGHKPTATDIKMPYNEAEN
KRSYHLCDLCDRIIIGDREWAAHIKSKSHLNQLKKRRLDSDAVNTIESQSVSPDHNK
EPKEKGSPGQNDQELKCSV"

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RATALIEDIFARDXIFIVVGGNYYIESILWKYLVNTKPQEMGTEVIDRKVELEKED
GLVLHKRLSQVDFEMAAKLBPHDKRKVARSLQVFEETGGISHSEFEHRQHTEEGGGFUG
GPLKFSNPCILWLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRYNQKNVSENSQD
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/db_xref="GI:21438848"
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Eutheria;
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               GGGATCCAGTTCAGGAGGGAGGGGTATGTTTGTCTCCCAGTCTGGGCAAAGGAGTGCTAT
                                            TTGAACCAACTGAAGAAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGT
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. 131 129.4 126.7 122. 119. 160. 160. 160 Score 788822 78862 78862 78862 78862 78862 Query Match 83122 159290 38400 161809 14486 167350 97005 201861 199863 21752 215711 228479 77304 201861 66680 79785 166496 200484 199863 181838 239888 198772 Length В AK074222 BC010741 AY052768 HS118J21 AC025002 AL354888 AC106650 AC093933 Ħ AX405704 Sequence AF074918 Homo sapi AK000068 Homo sapi AK074222 Homo sapi BC010741 Homo sapi BC019812 Mus muscu AL033527 Human DNA AC025002 Homo sapi AL1354888 Homo sapi AL1354888 Homo sapi AL1354888 Homo sapi AC106506 Mattus no AC039393 Rattus no AC03933 Rattus no AC03933 Rattus no AC103144 Rattus no AL354888 Homo sapi AC014105 Drosophil AC014105 Drosophil AC0103145 Rattus no AC103146 Rattus no AC103147 Particus no AC103147 Particus no AC103148 Rattus no AC103148 Rattus no AC103148 Rattus no AC103148 Rattus no AC103149 Drosophil AC103149 Drosophil AC103140 Drosophil AC103140 Drosophil AC103140 Drosophil AC103140 Drosophil AC103141 Rattus no AC103144 Rattus no AC103145 Rattus no AC103146 BHOMO sapi AC103147 Rattus no AC103148 Rattus no AC103140 Arabidops AB061403 Arabidops AR062600 Arabidops AR063210 Arabidops AP004813 Oryza sat AL022268 Streptomy AP005173 Oryza sat AE004123 Vibrio ch AC129717 Oryza sat AC113584 Tetraodon Description A98668 Sequence Arabidops Arabidops sequence 3

## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL	SOURCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 1 A98668 LOCUS
1 (bases 1 to 2041). Lemieux, J. and Heklmi, S. THE C. ELEGANS GRO-1 GENE Patent: WO 9910482-A 3 04-MAR-1999; LEMIEUX JASON (CA); UNIV MCGILL (CA)	unidentified unidentified unclassified	ce 3 from Patent WO99104821 GI:6781710	A98668 2041 bp DNA
			linear
			PAT
			PAT 26-JAN-2000

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 35 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 213691 bases at least Q30 Consensus quality: 215787 bases at least Q20
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Search completed: April 21, Job time: 444.109 secs
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                                                              Db 228584 TGTGACCTTTGTGATTGGATCATCATTGGGGACCAGGAATGGGCAGCACA 228633
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Best Local S
Matches 43
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                                                                                                                                             JOURNAL
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                                                                                                              Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 10, 2002 this sequence version replaced gi:20335375.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen,G., Chen,R., Chen,Z
Cleveland,C.D., Cox,C.,
                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                  Worley, K.C
                                                                                                                                                                                                                                   Unpublished
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                        Center project name: GEXO
Center clone name: CH230-172N14
-----Summary Statistics
Sequencing vector: Plasmid;
                                                                                     ------ Genome Center
Center: Baylor College of Medicine
Center code: BCM
Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 210507 bases at least Q40
                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Hemsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
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Nguyen,N., Nickerson,E., Nextson,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Parton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Stansey,J., Tang,H.,
Stansey,J., Tang,H.,
Stansey,J., Tang,H.,
Mang,S., Ward-Moore,S., Warren,R., Wasden,S., Wang,S.,
Wu,Y., Wu,Y., F., Zhou,J., Zorrilla,S., Nelson,D.,
Wu,Y., Wu,Y., F., Zhou,J., Zorrilla,S., Nelson,D.,
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Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Dannhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J.,
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Submitted (12-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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ox,C., Coyle,M.D., Dat
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AC106650.2 GI:21734730
                                                                                                                                                   Molecular and Human Genetics, Baylor College
ylor Plaza, Houston, TX 77030, USA
Jul 11, 2002 this sequence version replaced
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Rodentia;
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Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                               gi:18139174
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COMMENT

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Big Dye. Assembly program: Phrap; version O. Consensus quality: 115969 bases at Consensus quality: 12034 bases at Consensus quality: 127422 bases at
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45381: contig of 711 bp
5481: gap of 100 bp
46191: contig of 710 bp
6291: gap of 100 bp
46986: contig of 695 bp
7086: gap of 100 bp
47789: contig of 703 bp
7889: gap of 1700 bp
48590: contig of 701 bp
68590: gap of 100 bp
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41317: contig of 717 bp
1417: gap of 100 bp
42116: contig of 699 bp
2216: gap of 100 bp
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5727: gap of 100 bp
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34831: contig of 719 bp
331: gap of 100 bp
35627: contig of 696 hm
                  51.1%; Score 46; DB 2; Length 79; 100.0%; Pred. No. 5.7e-06; Live 0; Mismatches 0; Indels
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49414: contig of 724 bp
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50220: contig of 706 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw., SWISSRROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP
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On Jul 25, 2002 this sequence version
----- Genome Center
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Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-121J14 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          database can be found at
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Contact: humquery@sanger.ac.uk
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Best Local
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Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,T., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,T.M., Oilver,J., Peterson,K., Pierre,N.,
Plsani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Talamas,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (04-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 26, 2000 this sequence version replaced gi:7158126. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H. Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F. Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diaz, Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diaz, B., Cooke, P., DaArellano, K., Dewar, K., Diaz, Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Diaz, Collymore, A., Cooke, P., DaArellano, K., Dewar, K., Daarellano, K., Dewar, K., Diaz, Collymore, A., Cooke, P., DaArellano, K., Dewar, K., K., D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stange Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grand-Pierre, N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Homi
1 (Dases 1 to 79785)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 1, clone RP11-21702
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC025068.2 GI:7329438
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                             sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                  NOTE: This record contains 98 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 79785)
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                                                                                                                                                                                                                                                                                                                                  Center project name: L7716
Center clone name: 217_0_2
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               code: WIBR
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Pred. No. 2.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79785 bp
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LOW-PASS SEQUENCE
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will be sequenced to completion. In the event that
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171 8970; gap of 100 bp
171 8970; gap of 100 bp
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1237: gap of 100 bh

1237: gap of 100 bp

18 12237: gap of 100 bp

18 12950: contig of 713

13050: gap of 13751: contig of 713
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7 5593: contin
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1 1543: cc
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27562: contig of 713 bp in
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4776: co
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7105: gap of 100 bp
17825: contig of 720 bp in 1
77925: gap of 100 bp
18639: contig of 714 bp in 1
18739: gap of 100 bp
19457: contig of 718 bp in 1
                                                                                                                                                                                                                                                       100 bp

15372: contig of 720 bp

5472: gap of 100 bp

16183: contig of 711 bp in

283: gap of 100

17005:
                              26749: cc.
                                                                                                                     22709: contig of 714 br
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21069: contig of 700 bp in
69: gap of 100 bp
21895: contig of 726 bp in
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contig of 729 bp
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contig of 719 bp in
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64083 64182: gap of 100 bp

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72765 72864: gap of 100 bp

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86553 86652: gap of 100 bp

86653 93481: contig of 6829 bp in length

93482 93581: gap of 100 bp

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Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Trigilio,J.,
Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Autanam, Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beds, Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Changel v Collangelo, M. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200484 bp DNA linear Homo Sapiens chromosome 1 clone RP11-204L3 map 1, PROGRESS ***, 81 unordered pieces
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                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 14, 2000 this sequence version replaced gi:7770499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oilvar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Severy, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collin Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.
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                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name 
Center clone name:
                                                                                                                                                                                                                                                  Center: Whitehead Institute/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment:01170"
                                                                                                                                                                                                                                                                                                  Genome Center
                                                                          Project Information
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Pred. No. 2.3e-06;
0; Mismatches 8
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                                                                                                                                                                                                                                                  MIT Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *** SEQUENCING IN
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/note="12 repeat: matches 957. 2141 of consensus"
13474. 13591
/note="AluJo/FRAM repeat: matches 178. 295 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 27.
15137. .15215
/note="MIR repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="L2 repeat: matches 2129.
(4457. .14572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              te="L1MC3 repeat: matches 7071.
86. .14425
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20. .20782
                                                                                                                                     .dence=not_experimental
                                                                                                                                                                                                                              e="MIR repeat: matches no. .27733
                                                                                                                                                                                                                                                                                                                                                                                                                                              e="MIR repeat: matches 5. .71 of consensus"
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                                                                                                                                                     e="CpG island"
                                                                                                                                                                                     e="L2
                                                                                                                                                                                                                                                                                                                                                                                e="AluJo repeat: matches 2.8..24684
e="MIR repeat: matches 80.3..24891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="LTR16A repeat: matches 116. .325 of
e="MIR repeat: matches 81.
9. .31662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="AluSx repeat: matches 51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="AluSq repeat: matches 1.
9. .23381
e="MIR repeat: matches 132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="MIR repeat: matches 97. .262 of consensus"
                                                                                                                                                                                                             "MIR repeat: matches 37.
                                                                                                                                                                                                                                                                           e="MIR repeat: matches
                                                                                                                                                                                                                                                                                                         e="AluSp repeat: matches 143. .195 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =="LTR16A repeat: matches 60. .116 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em"AluSx repeat: matches 1.
7. .22073
                                                                                                                                                                                                                                                                                                                                                                  ="MIR repeat: matches 50. .199 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ="MIR repeat: matches 227.
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                              .31015
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.26275
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                                                                                                                                                                                                                                                                                                                               Insert size: 198363; sum-of-contigs
Insert size: 201159; 6.2% error; agarose-fp
Quality coverage: 3.87x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 189476 bases at least Q40 Consensus quality: 193311 bases at least Q30 Consensus quality: 195510 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (12-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestesanger.ac.uk
On Aug 21, 2000_this sequence version replaced g1:9213379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL354888.6 GI:9863692
HTG; HTGS_PHASE1; HTGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code:
                                                                                                                                                                                                                                                                                                                coverage: 3.98x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: bA473P22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Sanger Centre
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 199863)
                                                                                                 preserved.
                                                                                                                     soon as it is available and the accession number
2379 22743: c
22744 22843: gap
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    1 2278: contig of 2278 bp in length
2279 2378: gap of 100 bp
2379 22743: contig of 20365 bp in length
22744 22843: gap of 100 bp
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/note="AluSx repeat: matches 3.
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Pred. No. 2.2e-06;
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ne 1 clone RP11-473P22,
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2, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                             AL Submitted (18 FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 21, 1999 this sequence version replaced gi:6002299.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
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                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP1-118J721 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CpG Isi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HS118J21 166496 bp DNA linear PRI 18-FEB-2000 Human DNA sequence from clone RFI-118J21 on chromosome 1p34.1-35.3 Contains part of the gene for BMP8 (bone morphogenetic protein 8 (osteogenic protein 2)), an 1-myc-proto-oncogene, STSs, GSSs and CDG Islands.n, complete sequence
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HTG; BMPB; CpG Island; 1-myc; morphogenetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ellington, A.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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TSNQLLKKGIEALKQVTKRYARKQNRWVKNRPLSRPGPSVPPVYGLEVSDVSKWEESV
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/note="Vector: pC
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is the entire insert of clone RP1-118J21 The true
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Pred. No. 8.9e-17;
0; Mismatches 10
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right end of clone RPI-117L23 is at 38518 in this sequence. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl.
                                                                                                                                                                 /gene="BMP8"
/note=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matche 2764..2868 /note="FLAM_C repeat: matche complement(4214..4420)
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Sw:P18075 Tr:Q9YGH7 Sw:P23359
Sw:P34820 Sw:P34821"
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/note="MIR_repeat: matches 19.
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complement(join(949. .1098,3622. .3732,4242. .4321,
5153. .5347,14838. .14986,15379. .15568,28682. .29015))
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5153. .5347,14838. .14986,15379. .15568,28682.
/gene="BMP8"
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/note="MIR repeat: matches 57.
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QREILAVLGLPGRPRPRAPPAASRLPASAPLFMLDLYHAMAGDDDEDGAPAERRLGRA
DLVMSFVNMVERDRALGHQEPHWKEFRFDLTQIPAGEAVTAAEFRIYKVPSIHLLNRT
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/note-"match: CONAs: Em:S77477 Em:X51801 Em:M97017
Em:U39545 Em:J04566 Em:R80992 Em:M60316 Em:M60315
Em:M97016 Em:X56906 Em:AF100787 Em:U40034"
/note="match: STS:
10626. .12048
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/clone_lib="RPCI-1"
                                                                 /note="AluJb repeat: matches 1.
                                                                                                                                                                 /note="match: GSS:
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/osteogenic protein 2))"
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/db_xref="taxon:9606"
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Golovko, A. and Hjalm, G.
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GOLOVKO,A., Hjalm,G., Sitbon,F. and
Cloning of a human tRNA isopentenyl
Gene 258 (1-2), 85-93 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                   0564178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ProteIn_id="Cad34811.1"
/db_xref="G1:2143848"
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gplkfsnpcilmlhadqavlderldkrkvarsloyfeemgishberlrohteeggplg
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krsyhlcdlcdriitgdremaahikskshlnqlkkrrrldsdavntiesqsyspdhnk
epkekgspqnnoelkcgy"
549 t
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/product="tRNA isopentenylpyrophosphate transferase"
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/db_xref="dbEST:AA332152"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                                             /note="incompletely processed mRNA"
join(15. .829,917. .1505)
                                                                              /note="IPTase"
                                                                                                                                                    note="extension of sequence by 5' RACE"
                                                        'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates; Catarrhini; Hominidae;
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Pred. No. 8.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nicander, B.
transferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear PR
transferase
                                                                                                                                                                                                                                                                Uppsala,
                                                                                                                                                                                                                                                                                 Swedish University
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FEATURES

Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAK Plate: 41 Row: 1 Column: 20.

information can be found http://image.llnl.gov

source

/clone="MGC:30541 IMAGE:5042856"
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month old male mouse."

/map="FVB/N"

/db_xref="taxon:10090" /organism="Mus musculus" Location/Qualifiers

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REMARK
COMMENT
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SOURCE
ORGANISM
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BC019812
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VERSION
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BASE COUNT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1350
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (Lini)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
Contrologic Power (Contrological Power Contrological Power (Contrological Power (Contrological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC019812 2045 bp mRNA linear ROD 0 Mus musculus, RIKEN cDNA 2310075G14 gene, clone MGC:30541 IMAGE:5042856, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse
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                                                                                                                                                                                                                              Center code: BCM-HGSC
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SYHLCDLCDRIIIGDREWAAHIKSKSHLNQLKKRRRLDSDAVNTIESQSVSPDHNKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TALIEDIFARDKIPIVVGGTNYYIESLLMKYLVNTYPQEMGTEKVIDRKYELEKEDGL
VLHKRLSQVDPEMAAKLHPHKRKVARSJAVEETSISISEETLHRQHTEESGGPLGGP
LKFSNPCILMLHADQAVLDEELLDKKVADDMLAAGLLEELRDFHRRYNQKHVSENSQDY
HGIFQSIGFKEFHEYLITEGKCTLETSNQLLKKGIEALKQVTKRYARKQNRWVKNRFL
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QRLGGEIVSADSMQVYEGLDIITNKVSAQEQRICRHHMISFVDPLVTNYTVVDFRNRA
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Pred. No. 8.3e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2216;
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                     SGS
                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
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                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consorthim/LLML at: http://image.llnl.gov Series: IRAK Plate: 14 Row: p Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 701991
                                                                                                                                                                                                                                                                                                                                                                                            Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens, Similar to tRNA isopentenylpyrophosphate transferase, clone MGC:17002 IMAGE:3905836, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC010741.1 GI:14789610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC010741
                                                                                                                                                                                                                                                                                                                                                  Dickson, M.,
                                                                                                                                                                                                                                                                                                                                                                                      Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute, 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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/clone="COL01371"
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/note="cloning vector: page 337 c 408 g 46
                                       166.
                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
 /codon_start=1
/product="Similar
                                                                                     /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                                                                                                                                (Dickson, Mark) mcd@paxil.stanford.edu
4., Schmutz, J., Grimwood, J., Rodriquez,
                                                    'note="Vector:
                                                                                                                            'clone="MGC:17002 IMAGE:3905836"
                                                                           dat
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                                                                         host="DH10B"
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                                                                                                                      Sequence 119
AX405704
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THE C. ELEGANS GRO-1 GENE
Patent: WO 991048-A 3 OA-MAR-1999;
LEMIEUX JASON (CA); UNIV MCGILL (CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3 from A98668
Tang,Y.T., Liu,C.,
Xue,A.J., Yang,Y.,
                                                                 Homo sapiens
                                                                                                           AX405704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified
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                                        Mammalia;
                                                      Eukaryota;
                                                                                                                                                AX405704
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Lemieux,J. and
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                                       Eutheria;
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PALE I VQSF I QGHKPTAT PI KMPYNEA ENKRSYHLCDLCDRI I I GDREWAAH I KSKSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAH10741.1"
/db_xref="GI:14789611"
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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            Zhou, P.,
                                       Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Pred. No.
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Pred. No. 8.2e-23;
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W09910482
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             Asundi, V.,
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             Zhang,J.,
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               Zhao, Q.A.,
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Wehrman, T.

and Drmanac, R.T.

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                  NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA 11
                                                                        Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Deptment of Virology; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                 2 (bases 1 to 1749)
Sugano,S., Suzuki,Y., Ot
Shibahara,T., Tanaka,T.
Direct Submission
                                                                                                                                                                                                                                                        Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                   oligo capping; fis (full insert sequence).
Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL01383.
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21444833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKU00068 1749 bp mRNA line Homo sapiens cDNA FLJ20061 fis, clone COL01383
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KRRRLDSDAVNTIESQSVSPDYNKEPKEKGSPGQNDQELKCSV"
3 302 c 329 g 299 t
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CILMLHADQAVLDERLDKRVDDMLAAGLLEELRDFHRRYNQKNVSENSQDYQHGIFQS
IGFKEFHEYLITEGKCTLETSNQLLKKGPGPIVPPVYGLEVSDVSKWEESVLEPALEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="aravpvgsglrglQrTLpLvvILgaTgTgKsTLALQLgQrLggE
IVsaDsmQvyEgLDIITNKVsaQEQRICRHHMISFVDPLVTNYTVVDFRNRATALIED
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/product_"trNa !sopenteny! transferase"
/protein_id="AAL!4107.1"
/db_xref="GI:16209579"
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/db_xref="taxon:9606"
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T. and Nakamura,Y.
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TGTGACCTCTGTGATCGAATCATCATTGGGGAATGGGCAAGAGGCGCACATAAAAATCC 60
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                                           NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5'- 6 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AK074222.1 GI:186/6/65 oligo capping; fis (full insert sequence). oligo capping; fis (full insert sequence).
                                                                                                                                                                                                                    Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; Shirokane-dat, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                                                                                                                   Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                Sugano,S., Suzuki,Y., Ota,T., Obayashi,
Shibahara,T., Tanaka,T. and Nakamura,Y.
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                       Technology Agency)
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Run

AY052768 Homo sapi AK000068 Homo sapi AK074222 Homo sapi

Description

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Post-processing: Minimum Match 0%
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1308)
Lemieux, J., Lakowski, B., Webb, A., Meng, Y., Ubach, A., Bussiere, F.,
Barnes, T. and Hekimi, S.

Regulation of physiological rates in Caenorhabditis elegans by a
                                                                                                                     Homo sapiens tRNA isopentenyl to AY052768
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                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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transferase mRNA, partial cds.
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BC010741 Homo sapi A98668 Sequence 3 AV405704 Sequence AF074918 Homo sapi BC019812 Mus muscu AL033527 Human DNA AL354888 Homo sapi AC025068 Homo sapi AC025069 Rattus no AC103544 Rattus no AC103344 Rattus no AC103347 Rattus no AC103344 Rattus no AC103348 Homo sapi AF064864 Homo sapi AF064864 Homo sapi AL165283 Homo sapi AC107873 Hums muscu AC110331 Mus muscu AC110331 Mus muscu AC110331 Mus muscu AC105902 Homo sapi AC105902 Homo sapi AC105903 Rattus no AC105557 Rattus no AC105725 Papio cyn AC1030773 Papio cyn AC1030773 Papio cyn AC1030773 Papio cyn

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Search completed: April 21, 2003, 13:37:15 Job time :  $30.58\ \text{secs}$ 

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Matches 50; Conservative
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                                                                                                                This invention describes novel human nucleic acid segments (I) containing polymorphic sites. The polynucleotides of (I) are used for, e.g. correlating disease polymorphisms (or disease susceptibility) or other phenotypic traits (e.g. baldness, obesity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation, heart or central nervous system diseases; detecting susceptibility to microbial infection; treating or preventing such diseases; forensic analysis; gene therapy; paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning of the genes responsible); and the production of transgenic organisms. Antibodies raised against (I) are useful as diagnostic and therapeutic tools and in drug screening. AAH85144 - AAH87644 represent the human DNA sequences containing bialielic polymorphic sites described in the
                                                                                                                                                                                                                                                                                                                                                                                                                    Polymorphic human genomic sequences and related allele-specific probes and primers, useful for genetic analysis, e.g. diagnosis and monitoring of disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biallelic marker; polymorphism; human; disease; diagnosis; treatment; phenotypic trait; gene therapy; forensic; paternity; mapping; cancer; transgenic; single nucleotide polymorphism; SNP; ss.
                                                                       Sequence 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 261; 330pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-620443/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH87247 standard; DNA; 344 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (WHED ) WHITEHEAD INST BIOMEDICAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGGGAAGCAAGGAACCTTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGCAGCAGGAGAAGAAGAAGAAGGGA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATCCCACTTGAACCAACTGAAGAAAAGA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                       BP; 102 A; 82 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide polymorphism containing DNA sequence #2104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0057871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US06893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers replace(312,C)
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "single nucleotide polymorphism"
                29.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hudson T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.2%;
 Score 26.6; D
Pred. No. 5.8;
0; Mismatches
   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.3;
0; Mismatches
                                                                       87 G; 70 T; 3 other;
                                   DB
   39;
                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
   Indels
                                   Length
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Gaps
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2 GTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA 61

Query Match
Best Local Similarity
Matches 50; Conserv

Conservative

0,:

29.6%;

Score 26.6; Pred. No. 5 Mismatches

.8 DВ

39; 20;

Indels Length

0

Gaps

0

Sequence 344 BP;

102 A; 82 C; 87 G; 70 T; 3 other;

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RESULT 1
AAH87261
FTH XXX
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                                          This invention describes novel human nucleic acid segments (I) containing polymorphic sites. The polynucleotides of (I) are used for, e.g. correlating disease polymorphisms (or disease susceptibility) or other phenotypic traits (e.g. baldness, obesity, fertility, strength, response to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation, heart or central nervous system diseases; detecting susceptibility to microbial infection; treating or preventing such diseases; forensic analysis; gene therapy; paternity testing; mapping genomic loci associated with phenotypic traits (and subsequent cloning of the genes responsible); and the production of transgenic organisms. Antibodies raised against (I) are useful as diagnostic and therapeutic tools and in drug screening. AAH85144 - AAH87644 represent the human DNA sequences containing biallelic polymorphic sites described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biallelic marker; polymorphism; human; disease; diagnosis; treatment; phenotypic trait; gene therapy; forensic; paternity; mapping; cancer; transgenic; single nucleotide polymorphism; SNP; ss.
                                                                                                                                                                                                                                                                                      Claim 1; Page 263;
                                                                                                                                                                                                                                                                                                                                      Polymorphic human genomic sequences and related allele-specific probes and primers, useful for genetic analysis, e.g. diagnosis and monitoring
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-620443/53.
                                                                                                                                                                                                                                                                                                                                                                                                                          Lander ES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human single nucleotide polymorphism containing DNA sequence #2118.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9953095-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGGGAAGCAAGGACCTTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name=
                                                                                                                                                                                                                                                                                      330pp; English.
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                                                                                                                                                                                                                                                                                                                                       monitoring
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                                                                                   CC AAX10269-X12937 are human DNA fragments which contain biallelic CC polymorphic markers which have been isolated using the primers CC represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments CC can be used in methods for determining polymorphic forms in an individual CC can be used in methods for determining polymorphic forms in an individual CC can be used in methods for determining polymorphic forms in an individual CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, CC syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, CC familial hypercholesterolemia, polycystic kidney disease, hereditary CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary CC autoimmune diseases, inflammation, cancer, diseases of the nervous CC syndrome, osteogenesis imperfecta, acute intermittent porphyria, CC autoimmune diseases, inflammation, cancer, diseases of the nervous CC system, infection by pathogenic microorganisms, and characteristics such CC as longevity, appearance (e.g. baldness, obesity), strength, speed, CC endurance, fertility, and susceptibility or receptivity to particular CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid comments can also be used to produce medicaments for the treatment or problems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; phenotypic typing; characteristic; paternity testing; disease; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 162; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated nucleic acid segments from the human genome - used determining polymorphic forms for use in e.g. forensics, paterntesting or phenotypic typing for disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9820165-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-286974/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human biallelic polymorphic DNA fragment WI-8378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGACCTCTGTGATCGAATCATCATTGGGGGATCGCGAATGGGCAGCGCACATAAAATCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATACCAATGTTATCAAATGAGGTAAA
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                                                                        diseases
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57.0%;
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Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels

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Sequence

255

BP;

80 A;

63

<u>ე</u>

68 G;

42

T; 2 other

Query Match

Sequence

255

ВP;

80

A; 63 °C;

<u>و</u>

2 other;

29.6%;

Score 68

26.6; 42 T;

BB

19;

Length 255;

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                        AAX10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in AAX09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes inspidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, you willebrand's disease, tuberous sclerosis, hereditary
                                                 as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or
                                                                                                                      haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoLimnune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such
                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease
                                 prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-286974/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WHED ) WHITEHEAD INST BIOMEDICAL RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treatment; marker; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human biallelic polymorphic DNA fragment WI-8378b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX11457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX11457 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 CATGGCAGCAGGAGAAGAAGAAGAAGGAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGCCTCAGGAAGCTTATAATCATGGCAGAAGGCGAAGGGAAGCAAGGACCTTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGACCTCTGTGATCGATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50;
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                                                                                                                                                                                                                                                                                                                                                                                             Page 162; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                   such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0030455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                   diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 26.6;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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RESULT 11
AAT71696
ID AAT71
XX
AC AAT71
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AAT71699
ID AAT716
XX AAT71
XX 20-AU
DT 20-AU
DT 20-AU
DX HOMO
XX HEAL
XX HEAL
XX CLAIM
XX CLAIM
XX CLAIM
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                                                                                                                                                                                                                                                                                              4427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deaminase intron 2, which comprises 20303 base pairs from nucleotides 1964-22266 of the dCMP deaminase sense strand. The dCMP deaminase gene contains a 5, untranslated region (including the promoter), 5 exons, 4 introns and a 3, untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP to dUMP. Also, the dCMP gene can be altered (removed or mutated) to alter DNA replication in cells, which may lead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human deoxycytidylate deaminase intron 2 encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT71699 standard; DNA; 20303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1647
                                                                                                                                                                                     4487 ATACCAATGTTATCAAATGAGGTAAA 4512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding human deoxycytidylate deaminase recombinant deaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-244391/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant deaminase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT71699;
  AAT71696;
                                                       AAT71696 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20303 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes the human deoxycytidylate (dCMP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Column 83-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maley F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5622851-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HEAL-) HEALTH RES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                              TGACATTTTTCATTCCTTTTCTTTGTGGAATTCATTATAGTGAAGCACATTTAATCAAA 4486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCTATTCACACATTCATTAGGTGTCAGGTCTGTAAAGCAAAAATAAAATTCTAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCC
                                                                                                                                                                                                                                       ATCCCACTTGAACCAACTGAAGAAAA 88
                                                                                                                                                                                                                                                                                                                                                TGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maley GR,
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                       DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                        29.8%;
57.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Weiner KXB;
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                                                       26764 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 26.8;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽₽
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5052 G; 5682 T;
                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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The present sequence encodes the human deoxycytidylate (dCMP) deaminase gene, which contains a 5' untranslated region (including the promoter), 5 exons, 4 introns and a 3' untranslated region (including the stop signals). The gene can be used to produce recombinant dCMP deaminase, which can be used to convert dCMP Also, the dCMP gene can be altered (removed or mutated) to alter Dt Also, the dCMP gene can be altered (removed or mutated) to alter Dt
                                                                                                              DNA encoding human deoxycytidylate deaminase recombinant deaminase
                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                           exon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human deoxycytidylate deaminase gene
                                                                                                                                                                     Maley F, Maley GR,
                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant deaminase;
Sequence 26764 BP; 7079 A; 5521 C; 6539 G;
                                                                                           Claim 3; Column 55-78; 58pp; English.
                                                                                                                                          P-PSDB;
                                                                                                                                                                                                           10-JAN-1995;
                                                                                                                                                                                                                             10-JAN-1995;
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                  replication in
                                                                                                                                                                                        (HEAL-) HEALTH RES INC
                                                                                                                                         1997-244391/22
DB; AAW18205.
                  cells, which may lead to mutagenesis
                                                                                                                                                                                                           95US-0370975
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/number= 3
23741..23837
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25468..26764
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/number= 3
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                                                           A AKS4951 to AAK64702 encode the human immune/haematopoletic antigen (I) CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and CC treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC cancers and cancer metastases of haematopoietic antigen genomic CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
 Query Match
Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding useful for preventing, metastasis -
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                                                          Sequence 3616 BP;
                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID
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2000US-0246609.
2000US-0246610.
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2000US-0249613.
2000US-0249207.
2000US-0249209.
    30.2%; Score 27.2; Dilarity 58.8%; Pred. No. 6.7; Conservative · 0; Mismatches
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2000US-0250391
2000US-0251030
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2000US-0249214.
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                                                                                                                                                                                                                                                                                                                                                                                         human immune/hematopoietic antigen diagnosing and/or treating cancers
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                                                             784 G;
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                                                             977 T;
                                DB 22;
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                                                              other;
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polypeptides, and

29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 02-OCT-2000; 03-OCT-2000; 03-OCT-2000;

29-SEP-2000

13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000;

Length 3616; Indels

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RESULT 8
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                              New isolated nucleic acid genes from Drosophila and interactions
                                                                                                                                                                                                                          23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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 The invention relates to an isolated nucleic acid
                                Claim 1; SEQ ID
                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                         (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
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2000US-0614150.
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                           21pp + Sequence Listing;
                                                                           detection reagent for detecting 1000 for elucidating cell signalling and c
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Pred. No. 5.2;
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detection reagent
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; gene therapy; vaccine; metastasis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
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                                               14-AUG-2000;
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2000US-0180628.
2000US-0184664.
2000US-0186350.
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2000US-0190076
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Pred. No. 6.6;
0; Mismatches
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Best Local
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifty.wipo.int/pub/published_pct_sequences.
                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1776 BP; 491 A; 450 C; 464 G; 371 T; 0 other;
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                               31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (II). (II) is useful for generating antibodies against it,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                food supplement;
                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                          2001-639362/73.
DB; ABG03042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAACACACTGCAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGACCTCTGTTGTACACAAAGCCAGGGATATAGGGAAAAGGGGGAGAGGAAATATCCTCC 176
                                                                                                                                                                                                                                                                            RT, Liu C,
                                                                                                   SEQ ID No 3033; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-US08631
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2000US-0649167.
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                                                                                                                                                                                                                                                                            Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 27.6;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      forensic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIF at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                               22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; ds; prokaryotic antibiotic; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae DNA for cellular proliferation protein
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                                                                                                                                                                                Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-2000;
26-MAY-2000;
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                                                                                                            P-PSDB;
                                                                                                                                                                                                                                                (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                         27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                 23-OCT-2000;
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                                                                                                                                   2001-611495/70
                                                                                                              AAU38069
                                                                                                                                                                                                                                                                                          ; 2000US-191078P.
; 2000US-206848P.
; 2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-257931P.
; 2001US-269308P.
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                                                                                                                                                                                Ohlsen
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prokaryotic cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                   KL,
                                                                                                                                                                                                     Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 27.6; DB; Pred. No. 3.9; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug design
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                                                                                                                                                                                                        Wall D,
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                                                                                                                                                                                                          Trawick JD,
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                                                                                                                                                                                                          Carr GJ;
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Claim 27; Seq

ij

No 9565; 511pp; English

New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids

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Best Local
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome mapping; gene mapping; gene therapy; forensic; upplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                             IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human diagnostic protein
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                                                                                                                                                                                                                                                                                                                      103pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                              mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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RESULT 5
AAS64323
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce other types of data and products dependent on D amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published pct sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expension or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodypersity.
                                                                                              Claim 1; SEQ ID No 127; 103pp; English
                                                                                                                                                                                                                                                                      31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                      11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                              food
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS64323 standard; cDNA; 1776 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1248
                                                                                                                                                                                                  WPI:
                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS64323;
                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                      Homo
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                                                                                                                                                                                                2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATCCCACTTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGACCTCTGTTGTACACAAAGCCAGGGATATAGGGAAAGGGGAGAGGAAATATCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                             supplement;
                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping; gene mapping; gene therapy; upplement; medical imaging; diagnostic; genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                   ABG00136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel human diagnostic protein #127
                                                                                                                                                                                                                                                                      2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
                                                                                                                                                                                                                         TY
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; 289 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                          forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on DNA and
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique to restore normal activity of (II) or to treat disease states involving

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CCC XXXX PTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the human homologue of gro-1, and is referred to as hgro-1. The specification describes the five genes of the Generarhabditis elegans gro-1 operon (AAX36071). The operon contains the gro-1 gene (AAX36072), the gop-1 gene (AAX36075), the gop-2 gene (AAX36075), the gop-2 gene (AAX36077). The gro-1 gene can be used in a method for the diagnosis and/or prognosis of cancer in a patient. Transgenic mice containing a gene knock-out of a murine gene homologue of the gro-1 gene are useful as models of aging and cancer. The proteins encoded by the genes are useful for identifying compounds that affect the enzymatic activity of these proteins, in order to enhance longevity of a host and inhibit tumour formation. The gro-1 gene, together with the gop-1, gop-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for enhancing longevity formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2041 BP; 589 A; 421 C; 502 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                  neuroprotective; antiparkinsonian; protein expressed sequence tag; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                               Human; antianaemic; vulnerary; antiinflammatory; immunomodulator;
antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN59708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABN59708 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gop-3 and hap-1 genes enables study of a physiological clock
                             Claim 1;
                                                                                                                                                             Tang YT,
                                                                                                                                                                                          (HYSE-) HYSEQ INC
                                                                                                                                                                                                                     11-SEP-2000;
                                                                                                                                                                                                                                                  10-SEP-2001; 2001WO-US26015
                                                                                                                                                                                                                                                                               21-MAR-2002
                                                                                                                                                                                                                                                                                                           WO200222660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human coding sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2002
                                                      An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                  WPI; 2002-292408/33.
                                                                                                    P-PSDB; ABB97295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGTGACCTCTGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATCCCACTTGAACCAACTGAAGAAAAAGA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAATCCCACTTGAACCAACTGAAGAAAAGA 1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGACCTCTGTGATCGAATCATCGTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
Similarity 100.0%;
                                                                                                                                              Yang
                                                                                                                                                           Liu
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                                                                                                                                                                                                                       2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                             ID NO 119;
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                                                                                                                                               Wehrman
                                                                                                                                                             Zhou P,
                             509pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2130
                                                                                                                                              Asundi V,
T, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                               ndi V, Zhang
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NO: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     host and inhibiting tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6e-23;
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                                                                                                                                                                                                                                                                                                                                                                                    rheumatic; gene therapy;
apy; EST;
                                                                                                                                                              Zhao
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The present invention

provides the

protein and

coding sequences

AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The pre invention also describes a method of detecting differentially exp

Claim 1;

Page 399; 1097pp; English.

Polynucleotide library used to determine

cancerous

states

of mammalian

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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1271
                                                                                                                                                                              15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkinson's disease. The present sequence is a coding sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA00911 standard; cDNA; 300
                                 Williams LT, Escobedo
Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                     oestrogen receptor-negative breast cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000
WPI; 2000-126369/11.
                                                                                                                                                                                                                                                   14-MAY-1998;
                                                                                                                                                                                                                                                                                        13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                             W09958675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer;
                                                                                                                         (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                            18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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les 90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATCCCACTTGAACCAACTGAAGAAAAGA 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      colon cancer; tumour; diagnosis; gene expression product;
detection; cancerous state; metastasis; identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     oestrogen receptor-positive breast
                                                                                                                                                                                                98US-0085696.
98US-0105234.
                                                                                                                                                                                                                                    98US-0085426.
98US-0085537.
                                                                                                                                                                                                                                                                                        99WO-US10602.
                                                                                                                                                                                 98US-0105877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell line polynucleotide sequence
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                               J, Innis MA, Garcia PD, Sudduth-Kli
Randazzo F, Kennedy GC, Pot D, Kass
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                           Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:902
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                                                                          Kassam
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-513-151-3_COPY_1121_1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.3 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn~emb1/NA1980.DAT:
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \times \footnote{\gamma} \text{geneseq/geneseqn-embl/NA1989.DAT:* \footnote{\gamma} \text{gendata/geneseq/geneseqn-embl/NA1999.DAT:* \footnote{\gamma} \text{SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:* \footnote{\gamma} \text{SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:* \footnote{\gamma} \text{SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:* \footnote{\gamma} \text{SIDS2/gcgdata/geneseq/geneseq-geneseq-geneseq-geneseq-geneseq-ge
                                                                                                                                                                                                                                                                                                                                                                                                              Length DB
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ABN59708
AAA00911
AAS67227
                                                                                                                         AAS64323
AAS67229
AAK76334
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                                                                                                                                                                                                                                                                                                                                                                                                 Description
                     DNA encoding novel Streptococcus pneu Drosophila melanog
                                                                                                                                                                                                                            Human homologue of
Novel human coding
Human colon cancer
                                                                                                                                              DNA encoding novel
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## ALIGNMENTS

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RESULT 1
AAX36073
.ID AAX3
XX AAX3
XX Huma
XX Huma
XX Gro-
KW App-
XX Homc
XX Hom

Molecular identity of the gro-1 gene - useful for cancer diagnosis and/or prognosis, and where compounds affecting encoded proteins a
                                                                                                                                               WPI; 1999-190615/16.
                                                                                                                                                                                                                                     Barnes T,
                                                                                                                                                                                                                                                                                                                          (UYMC-) UNIV MCGILL.
                                                                                                                                                                                                                                                                                                                                                                                                                     25-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX36073 standard; DNA; 2041 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gro-1 operon; gro-1 gene; gop-1 gene; gop-2 gene; gop-2 gene;
hap-1 gene; cancer; aging; longevity; tumour formation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human homologue of gro-1, referred to as hgro-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX36073;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physiological
                                                                                                                                                                                                                                Hekimi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clock;
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                                                                                                                                                                                                                                Lemieux
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2472 AATCTTCCTTCATTTCAACTGATATGGTATCATCATAGTCAATTTCCTCTTGATCTG 2413

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US-09-364-862-14/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-09-470-618-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-470-618-14/c
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Best Local Similarity 58.3
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 14
LENGTH: 4999
                                                                                                      SOFTWARE: PatentIn Ver. SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09470618
                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/364, CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-07-74
                                                                                                                                                NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                     equence 14, Application US/09364862
atent No. 6221349
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                                                                                                                                                                   EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                       TTLE OF
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PPLICANT: Colosi, Peter C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARLIER APPLICATION NUMBER: 60/
                                          ORGANISM: Artificial Sequence
                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: CELLS ILE REFERENCE: AVIGEN-03743
                                                                                                                                                                                                                                                                                                                                                                                                                    NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URRENT APPLICATION NUMBER: US/09/470, 
URRENT FILING DATE: 1999-12-22
ARLIER APPLICATION NUMBER: 09/364,862
ARLIER FILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: Couto, Linda B. PPLICANT: Colosi, Peter C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NERAL INFORMATION:
OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2819 AATCTTCCTTCTTCAACTGATATGGTATCATCATAGTCAATTTCCTCTTGATCTG 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
TILE OF INVENTION: by Target Cells
                                                                                       ENGTH: 4999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2759 ACTGAAGAGTAG 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LE REFERENCE: Avigen-0408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2412 ACTGAAGAGTAG 2401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 ACTGAAGAAAAG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAACCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/364,862 FILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                 INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII INVENTION: BY TARGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/125,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
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Pred. No. 11;
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  Synthetic
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US-09-364-862-14

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Query Match 26.7%; Score 24; DB 4; Length 4999; Best Local Similarity 58.3%; Pred. No. 11; Matches 42; Conservative 0; Mismatches 30; Indels 0;
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18 AATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTGAACCA 77

2819 AATCTTCCTTCATTTCAACTGATATGGTATCATAGTCAATTTCCTCTTGATCTG 2760

Qy 78 ACTGAAGAAAAG 89

2759 ACTGAAGAGTAG 2748

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Search completed: April 21, 2003, 16:30:12 Job time : 12.3078 secs

FILING DATE:

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US-08-961-527-210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08484891 Patent No. 5935935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                    TELEFAX: 201-994-1744
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6453 AAGACGACGTGAAAGAAGTGACAAA 6477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6393 GTGTTATCCGTGATGGTGTCGTTATCTATGATGGTGAACTCGCAAGCTTGAAACACTATA 6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION:
                                                                                  NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 27.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                    APPLICATION NUMBER: 08/218,335
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: 08/074,920
FILING DATE: 10-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: 014545 Elifot MELTICATION:
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect : CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 AATCCCACTTGAACCAACTGAAGAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/484,891 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Roseland
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Carella, Byrne, Bain, Gii
ADDRESSEE: Cecchi, Stewart & Olstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaleko, Michael
Smith, Theodore
                                                                     201-994-1744
                                                                                                                                                                                                                                                                                                                                                     SYSTEM: MS-DOS WordPerfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                        inch diskette
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Pred. No. 1
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RESULT 13
US-08-717-294-41/c
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   Best Loc
Matches
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Best Local Similarity 58.3%;
Matches 42; Conservative
                               Query Match
                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2386
                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                             NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-SEP-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAACCA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 ACTGAAGAAAAG 89
                                                                                                  STRANDEDNESS:
               Local
                                                                                           TOPOLOGY:
                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 20-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                   ENGTH:
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              Similarity
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                                                                                                                                     4670 base pairs
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                                                                                                                                                                                                  617-428-7045
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HAAS, JURGEN
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   Conservative
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                                                                                           linear
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               26.7%;
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Score 24; DB 3; Pred. No. 10; 0; Mismatches 3
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                                Length 4670;
   Indels
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TELEFAX:

610-407-0701

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                             Query Match
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Best Local Similarity 62.9
Matches 39; Conservative
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                                                                                                                                                              NFORMATION FOR SEQ ID NO:
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tent No. 6146845
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MEDIUM TYPE: Diskett
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                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
                                                                       MOLECULE TYPE:
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/0 FILING DATE: 02-APR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Staloadhesin Fa
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 CC 308
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                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 TCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAATCCCACTTGAA 74
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                                                                                  STRANDEDNESS: SI
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                                                                                                                                                                                                                                                 NAME: PRESTIA, PAUL F
REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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nucleic acid
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Pred. No. 2.4;
               Score 25.2;
Pred. No. 3
Mismatches
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US-08-961-527-210
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 2787
TYPE: DNA
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GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 60/079,770
EARLIER FILING DATE: 1998-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Camilli, Andrew
TITLE OF INVENTION: SYSTEMATIC IDENTIFICATION OF ESSENTIAL
TITLE OF INVENTION: GENES BY IN VITRO TRANSPOSON MUTAGENES:
FILE REFERENCE: 00742/052002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Akerley, Brian J.
APPLICANT: Rubin, Eric J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS: """ FOR THE CORRESPONDENCE OF 
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 CC 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AATCCCACTTGAACCAACTGAAGAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 CC 76
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                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                           COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VECCEMBERS OPERATIONS SYSTEM: MSDOS VECCEMBERS OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 47; Conserv
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Rockville
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30, 620738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maryland
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9410 Key West Avenue
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Pred. No. 7.1;
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GENERAL INFORMATION:

Burnham,

Magdalena Martin K.

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Ingraham,

Alison F.

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                                                                                                                ; OTHER INFORMATION: Synthetic B.t. toxin US-09-178-252-7
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Matches
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                                                    Matches
                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                     EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stelman, Steven J
APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/574,912
CURRENT FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/283,763
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/105,985
PRIOR FILING DATE: 1999-10-28
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                                                                                                                                                                                                                                                                                                                                                                          IITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                      LENGTH: 1815
TYPE: DNA
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                                                                                                                                                      FEATURE:
                                                                                                                                                                    ORGANISM: Artificial Sequence
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tent No. 6218188
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                                                                  Local
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3 TGACCTCTGTGATCGATCATTGGGGATCGCGAATGGGCAGCGCACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              David J.
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Pred. No. 1
                                                               Score 25.4;
Pred. No. 2.
                                                  Mismatches
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EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1998-03-02 NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stelman, Steven J.
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                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                            SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
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ADDRESSEE: RATNER & PRESTIA
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REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 19482
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                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                                                                                                            APPLICATION NUMBER:
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35; Conservative
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                                                  PRESTIA, PAUL F
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                                                                                                                                                                                                                                                                                                                  USA
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PENTION: Sialoadhesin Family Member-2
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                                                                                                                                                                                                                                                                 Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAF-2)
                                                                                                                                                                                                              for Windows Version
                                                                                                       60/041,886
                                                                                                                                                                            US/09/038,832
                   GH-50018
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Pred. No. 2
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Patent No. 562285
                                                                               Sequence 93, Application US/09484970B Patent No. 6426186
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4427 TGACATTTTTCATTCCTTTTTCTTTGTGGAATTCATTATAGTGAAGCACATTTAATCAAA 4486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Maley, Frank APPLICANT: Maley, Gladys F.
                                                                                                                                                                                                                                                    6390 TGACATTTTTCATTCCTTTTTTTTTTGTGGAATTCATTATAGTGAAGCACATTTAATCAAA 6449
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (9
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Timian, Susan J
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                   6450 ATACCAATGTTATCAAATGAGGTAAA 6475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                   63 ATCCCACTTGAACCAACTGAAGAAAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 10-JAN-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDRESSEE:
                                                                                                                                                                                                                                                                                    3 TGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
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                             Jones, Kas
Volkmuth,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (716)263-1600
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nixon, Hargrave, Devans & Doyle
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                                                 Karen A.
                 Michael
BONE REMODELING GENES
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Pred. No. 1.
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US-09-574-912-1
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; TYPE: DNA
; ORGANIZM: Streptococcus pneumoniae
US-09-283-763-1
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US-09-283-763-1
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SEQ ID NO 93
LENGTH: 3446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Sequence 1, Application US/09574912 Patent No. 6399343
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                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER FILING DATE: 1999-10-28 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/105,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/283,763
CURRENT FILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: So,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brown, James R.
APPLICANT: Ingraham, Karen A.
APPLICANT: Chalker, Alison F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Warren, Richard L
APPLICANT: Mathie, Thomas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holmes, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Incyte ID No. 6426186 252234.3CB1
NAME/KEY: unsure
LOCATION: 1432, 1435
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLICANT: Biswas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICANT: Burnham, Martin K. R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Traini, Christopher M.
                                                                                                                                                                     2615 GTGTTATCCGTGATGGTGTCGTTATCTATGATGGCGAACTCGCAAGCTTGAAACACTACA 2674
                                                                                                  2675 AAGATGACGTGAAAGAAGTGACAAA 2699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AATCCCACTTGAACCAACTGAAGAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LE OF INVENTION: infB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 GCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAG 89
                                                                                                                                                                                                                                      Local Similarity es 48; Conserv
                                                                                                                                                                                                     2 GTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION
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76.2%;
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                                                                                                                                                                                                                                                                    DB 3;
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Post-processing: Minimum Match 0%
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Maximum DB
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-277-565-27

US-08-961-527-210

US-08-484-891-7

US-08-717-294-41

US-09-470-618-14

US-09-364-862-14

US-09-364-862-14

US-09-283-1

US-08-288-107-1

US-08-281-202-1

US-08-211-202-1

US-08-211-202-1

US-08-364-851A-1

US-08-364-0048-3

US-08-251-937A-3

US-08-251-937A-3

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US-09-178-252-7

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US-08-370-975B-1
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6407.139 Million cell updates/sec
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	ALIGNMENTS	US-09-426-290-1	US-09-813-133A-3	US-08-811-177A-1	US-09-171-209-73	US-09-676-610B-24	US-08-852-807-1	US-08-852-807-12	US-07-853-913-1	US-09-178-252-1	US-09-178-252-3	US-09-364-862-13	US-09-470-618-13	US-08-683-839B-2	PCT-US94-13200-1	PCT-US93-03275-3	US-09-523-656-1	US-09-315-179-1	US-09-037-601-1	
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TELEFAX: (716)263-1600
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20303 base pai
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                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 4q35
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,975B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maley, Frank
APPLICANT: Maley, Gladys F.
APPLICANT: Weiner, Karen X.B.
TITLE OF INVENTION: Human Deoxycytidylate
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                         TELEPHONE: (716)263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10
CLASSIFICATION:
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STATE: New York
                                                                                                                                                                                 H: 20303 base pairs nucleic acid
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                                                                                                                                                                                                                                                        (716)263-1636
(716)263-1600
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                    29.8%;
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Score 26.8; DB Pred. No. 1.5; 0; Mismatches
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PRIOR FILING DATE: 1999-03-
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 212
LENGTH: 1529
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-302-212
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; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT APPLICATION data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1128
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-860-1128
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Search completed: April 21, 2003, 18:47:45
Job time: 13.3895 secs
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US-09-925-302-212
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Best Local Similarity 63.3%;
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Best Local Similarity 56.0%;
Matches 47; Conservative
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 403 CTCTGCCTCCCAAGCCCTTCTCATGTGGGCGGAGTGGAAAGGGACATAAAAGGAAATCCC 462
                                                                            463 CATTTGGAAGTACAGAAAGAAAGA 486
                                                                                                    67 CACTTGAACCAACTGAAGAAAAGA 90
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Pred. No. 20;
0; Mismatches
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Pred. No. 14;
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US-09-972-714-2,

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US-09-910-600-5/c
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; ORGANISM: Homo sapiens
US-09-972-714-2
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-910-600-5
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RESULT 12
US-09-972-714-9/c
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Best Local 9
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LENGTH: 502
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Patent No. US20020106738A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FOUSSIAS, GEORGE
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: NOVEL SIGLEC GENE
FILE REFERENCE: 11757.56USU1
CURRENT APPLICATION NUMBER: US/09/972,714
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/239,007 PRIOR FILING DATE: 2000-10-06
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PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/910,600 CURRENT FILING DATE: 2001-07-20
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APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
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Pred. No. 14;
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Pred. No. 9.1;
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TYPE: DNA
CORGANISM: Homo sapiens
US-09-972-714-9
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, TYPE: DNA
, ORGANISM: Homo sapiens
US-09-972-714-1
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APPLICANT: Diamandis, Eleftherios
APPLICANT: Diamandis, Eleftherios
TITLE OF INVENTION: NOVEL SIGLEC GENE
FILE REFERENCE: 11757.56USU1
CURRENT APPLICATION NUMBER: US/09/972,714
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: US 60/239,007
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 15
RESULT 14
US-09-764-860-1128
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US-09-972-714-1/c
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Best Local
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Pred. No. 14;
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Pred. No. 23;
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

Sequence 1128, Application US/09764860 Patent No. US20020094953A1

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US-09-764-869-2256
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SEQ ID NO 2256
LENGTH: 4346
                                                                                                           Query Match
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Best Local :
                                                                         Matches
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                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
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TITLE OF INVENTION: Nucleic Acids, Proteins,
                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/178,252
PRIOR FILING DATE: 1998-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cardineau,
                                                                                                                                                             OTHER INFORMATION: Synthetic B.t. toxin
                                                                                                                                                                                FEATURE:
                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                    URRENT APPLICATION NUMBER: US/09/826,660
                                                                                                                                                                                                                                     ENGTH: 1815
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLICANT: Narva, Kenneth E.
TLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
LE REFERENCE: MA-714XC2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4138 GAACCTAAAATCCTGGTCCCACCTGAGCCAAGTGAAGAGAGGG
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                                                                                                                                                                                                                                                          ID NO 7
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                      TGACCTCTGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACAT 53
TGATGGCTGTGATCAAAGCATCATCTGTGTTAGCAAAGCGTATGCGCACAT
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32; Conserv
                                                                                          Similarity
                                                                                                                                                                                                                                                                           PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stelman, Steven J.
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76.2%;
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                                                                                      Score 25.4;
Pred. No. 12;
                                                                     Mismatches
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                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1375
                                                                                                                                       Query Match 28.0%;
Best Local Similarity 62.9%;
                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1375, Application US/09969373 Patent No. US20020133852A1
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                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods
FILE REFERENCE: 38-10(52679)A
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/760,427 PRIOR FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/065,215
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR FILING DATE: 1998-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/178,252 PRIOR FILING DATE: 1998-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins FILE REFERENCE: MA-714XC2D1
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APPLICANT: Stelman, Steven J.
                                                                                                                                                                                                                                   LENGTH: 182
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic B.t. toxin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1815
TYPE: DNA
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             73 AA 74
                                                  82 GAATGAATAATCATTAGATCTTATGAATGGTTAATGTTAAAAATACCAAAATCCCACGTC 23
                                                                       13 GATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTG 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                                                                                                                          Conservative
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Pred. No. 6.3;
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Pred. No. 12;
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9565, Application US/09815242 o. US20020061569A1

Haselbeck, Robert

Ohlsen, Kari L. Zyskind, Judith W

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US-09-815-242-9565
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SEQ ID NO 9565
LENGTH: 2703
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Best Local (
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                                                SOFTWARE: PERL Program
SEQ ID NO 41
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                                                                                                                                                                                                                                           Patent No. US20020077470A1
GENERAL INFORMATION:
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LOCATION: (1).
                                                                                                     CURRENT APPLICATION NUMBER: US/09/880,192
CURRENT FILING DATE: 2001-06-12
                                                                                                                                                                      APPLICANT: Volkmuth, Wayne APPLICANT: Klingler, Tod M. APPLICANT: Azimzai, Yalda
                                                                                                                                    TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION FILE REFERENCE: PB-0009-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                       2525 GTGTTATCCGTGATGGTGTCGTTATCTATGATGGCGAACTCGCAAGCTTGAAACACTACA 2584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GTGACCTCTGTGATCGATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCA 61
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                                                                                                                                                                                                                                                                                                                                                                    AAGACGACGTGAAAGAAGTGACAAA 2609
                                                                                                                                                                                                                                                                                                                                                                                                    AATCCCACTTGAACCAACTGAAGAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                    3441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 2
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US-10-091-504-2256

Sequence 2256, Application US/10091504

US20030059908A1

Publication No. US20 GENERAL INFORMATION:

Prior Application removed -SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2256 LENGTH: 4346

ORGANISM: Homo sapiens 10-091-504-2256 CURRENT APPLICATION NUMBER: US/10/091,504 CURRENT FILING DATE: 2002-03-07 NUMBER OF SEQ ID NOS: 2442

See File Wrapper or Palm

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC007Cl

and Antibodies

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; OTHER INFORMATION: Incy
US-09-880-192-41
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                                                                  Query Match
Best Local S
Matches 32
                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 126
LENGTH: 3444
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                                                                                                                                                                                                                                                          CÜRRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                              APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: GENETICS INSTITUTE, INC.
APPLICANT: GENETICS INC.
APPLICANT: CARLENGE ENCODING THEM
FILE REFERENCE: GI 6000-10A
                                                                                                                                                                         TYPE: DNA
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809 GAACCTAAAATCCTGGTCCCACCTGAGCCAAGTGAAGAGAGG 850
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                                48 GCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAAG 89
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32; Conser
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LaVallie, Edward R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treacy, Maurice
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                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kenneth
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76.2%;
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Pred. No.
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  length: 0
length: 2000000000
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1: /cgn2_6/ptodata/2/pubpna/US07.
2: /cgn2_6/ptodata/2/pubpna/ECT_1.
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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US-09-972-714-9

US-09-972-714-1

US-09-972-714-1

US-09-974-860-1128

US-09-925-302-212

US-09-764-864-1593
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US-09-815-242-9565
US-09-880-192-41
US-10-114-893-126
US-10-091-504-2256
                                                                                                                      US-09-764-869-2256

US-09-826-660-7

US-09-826-660-8

US-09-966-660-9

US-09-969-373-1375

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8702.120 Million cell updates/sec
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_NEW_PUB.seq:*
     Sequence 3043, Ap

Sequence 417, Appl

Sequence 126, Appl

Sequence 2256, Ap

Sequence 2256, Ap

Sequence 27, Appl

Sequence 1375, Ap

Sequence 1375, Appl

Sequence 2, Appl

Sequence 2, Appl

Sequence 3, Appl

Sequence 1128, Ap

Sequence 1128, Ap

Sequence 1128, Ap

Sequence 1128, Ap

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Sequence 17, Appli
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# ALIGNMENTS

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; SEQ ID NO 3043

; LENGTH: 2000

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

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RESULT 2
US-09-815-242-9565
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US-09-938-842A-3043
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAININ
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR PILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-06-22
                                                                                        397
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                                                                                                               62 AATCCCACTTGAACCAACTGAAGAA 86
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                                                                                        CATCTCTCTCACGCAGATGACAAA 421
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57.6%; Pred. No. 2.3;
Live 0; Mismatches
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RESULT 14
US-09-898-888-8140/c
; Sequence 8140, Application US/09898888
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                                                                      ; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-898-888A-8140
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: Sequence 8140, Application US/09898888A
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8140
LENGTH: 1041
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GENERAL INFORMATION:
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Query Match 100.0%; Score 90; DB 33; Best Local Similarity 100.0%; Pred. No. 1.5e-21; Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                        SEQ ID NO 8140
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CURRENT APPLICATION NUMBER: US/09/898,888
CURRENT FILING DATE: 2001-07-03
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                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US 09/205,070
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA TITLE OF INVENTION: LIBRARIES FILE REFERENCE: 20411-748CON1 CURRENT APPLICATION NUMBER: US/09/898,888A CURRENT FILING DATE: 2001-07-30
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863 AAATCCCACTTGAACCAACTGAAGAAAAGA 834
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                  AAATCCCACTTGAACCAACTGAAGAAAAGA 90
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Search completed: April 21, 2003, 17:14:11 Job time: 267.819 secs

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US-09-359-922-3465/c
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; ORGANISM: Homo sapiens
US-09-359-922-3465
                               Sequence 3465, Application US/09919002
GENERAL INFORMATION:
APPLICANT: Leshkowitz, Dena
APPLICANT: Liu, Jin
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
TITLE OF INVENTION: LIBARRIES
FILE REFERENCE: 20411-752CON1
CURRENT APPLICATION NUMBER: US/09/919,002
CURRENT FILING DATE: 2001-07-30
CURRENT FILING DATE: 2001-07-30
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EARLIER FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
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EARLIER APPLICATION NUMBER: US
EARLIER FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 13203
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CURRENT FILING DATE: 1999-07-22
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APPLICANT: Liu, Jin
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ENGTH: 1039
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90; Conserv
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APPLICATION NUMBER: DATE: 1999-07-22
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Pred. No. 1.5e-21;
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Pred. No. 1.5e-21;
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US-09-340-623-8140/c
; Sequence 8140, Application US/09340623
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; SEQ ID NO 8140
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-205-070-8140
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105-09-205-070-8140, Application US/09205070
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; LENGTH: 1041
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-340-623-8140
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Matches
                                                                              SEQ ID NO 8140
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Best Local Similarity
Matches 90; Conserv
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                                                                                                              TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA TITLE OF INVENTION: LIBRARIES FILE REFERENCE: 20411-7484CON1 CURRENT APPLICATION NUMBER: US/09/340,623 CURRENT FILING DATE: 1999-06-28 EARLIER APPLICATION NUMBER: US 09/205,070 EARLIER FILING DATE: 1998-12-03 UNMBER OF SEQ ID NOS: 45207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/205,070 CURRENT FILING DATE: 1998-12-03 NUMBER OF SEQ ID NOS: 45207
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TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748
                                                                                                  SOFTWARE:
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No.
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Pred. No. 1.5e-21;
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1.5e-21;
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; FEATURE:
NAME/KEY: misc_feature
; LOCATION: (1)...(442)
; OTHER INFORMATION: n = A,T,C or G
US-09-515-128-21383
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RESULT
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21383
LENGTH: 442
                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                 Matches
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CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: 09/034,341
EARLIER FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From a cDNA Library of Fetal Liver-Sp. FILE REFERENCE: 728CIP
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 208
                                                90;
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: Yang, Fei
: Yim, Kenneth
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Tran, Lien
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Asghari, Vida
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Giedt, Gretchen
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Faulkner, Brandy
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Smith, Benjamin
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Palencia, Servando
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Iguyen, Phuong
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                                                                                                                                                                                 Conservative
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Pred. No. 1.2e-21;
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                                                                                                                                                                                                               Length 442;
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                                                                                                                   RESULT 9.
US-09-359-922-3465/c
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PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 24489
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21383
             Sequence 3465, Application US/09359922
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS cDNA
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-752CON1
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Best Local S
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APPLICANT: Arterburn, Macı
Asahari, Vida
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CURRENT FILING DATE: 2000-11-21
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TYPE: DNA
ORGANISM: Homo saplens
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     CURRENT APPLICATION NUMBER: US/09/359,922
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NAME/KEY: misc_feature
LOCATION: (1)...(442)
OTHER INFORMATION: n = A,T,C
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Yang, Fei
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Yim, Kenneth
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Giedt, Gretchen
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Faulkner, Brandy
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Nogra, Margie
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Tkach, Joe
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                                                        SOFTWARE: PER
SEQ ID NO 9519
LENGTH: 289
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                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/532,315 CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                    Prior application data removed • refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 42212
                                                                                                                                                                                                                                                                                                          FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
NAME: CERRONE, MICHAEL C.
NAME: CONTROL OF 
                                                                                                                                                                                                                                                                                                                                  IPPLICANT: Naughton, Rebecca E.

ITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPLICANT:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 263 base pairs
DRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94904
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/044,082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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                                                                                                                                 PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                        Mullahy, Sara J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Stuve, Laura L
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Delegeane, Angelo M.
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Pred. No. 1e-21;
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; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo s
US-09-943-143-7332
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                                                                                                                          SOFTWARE: Hy-patent.pl Version 3.1 SEQ ID NO 7332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/489,036
CURRENT FILING DATE: 2000-01-19
NUMBER OF SEQ ID NOS: 35324
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 7332
LENGTH: 372
TYPE: DNA
                                                                                                                                                                                                                                                                                               Sequence 7332, Appli GENERAL INFORMATION:
   Matches
                                 Query Match
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Best Local Similarity
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                                                                                                                                                     PRIOR FILING DATE: 200 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/943,143
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/489,036
                                                                                                                                                                                                                                APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 783
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   Local Similarity les 90; Conserv
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   Conservative
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                Score 90;
Pred. No. 1
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Pred. No. 1.1e-21;
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Pred. No.
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                              Length 372;
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Indels
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Gaps
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72.4 72.4 55.4 52.8 47.2 47.2

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RESULT 1
US-09-056-942-268
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                            TELEFAX: (415) 845-4166
NFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
                                                        ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0357P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYNUCLEOTIDES TITLE OF INVENTION: HUMAN FETAL LUNG NUMBER OF SEQUENCES: 2102
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                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 POI
CITY: PALO ALTO
STATE: CALIFORN
                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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Delegeane, Angelo M.
Naughton, Rebecca E.
Klingler, Tod M.
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                                                                                                                                                                                                                                                                                                                                                                     USA
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Ito, Laura Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gooding, Douglas H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM
                                                                                                                                                                                                                                      US/09/056,942
                                                                                                                                                                        60/044,082
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US-10-097-340-152
US-09-652-124-7628
US-08-810-326-938
US-08-810-326-938
US-60-012-699-938
US-60-012-699-938
US-60-9151-199-3234
US-09-151-199-3234
US-09-151-965-1320
US-09-182-965-1320
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US-09-513-151-3
US-60-172-360-26034
US-10-133-013-165
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PCT-US02-07826-150
PCT-US02-07826-152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 150, App
Sequence 152, App
Sequence 150, App
Sequence 152, App
Sequence 938, App
Sequence 938, App
Sequence 2119, App
Sequence 2119, App
Sequence 1320, App
Sequence 46638, App
Sequence 1079, App
Sequence 1079, App
Sequence 33691, App
Sequence 3601, App
Sequence 3617, App
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Sequence 3, Appli
Sequence 26034, A
Sequence 165, App
Sequence 33690, A
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US-60-044-082-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 42212
SOFTWARE: PERL Program
SEQ ID NO 9510
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9510, Appli
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                             Sequence 268, Application:
                                                                                                                                                                                                                                                                                                                        Matches
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Best Local S
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CURRENT FILING DATE: 2000-03-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR
FILE REFERENCE: PD-1002 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure
LOCATION: 228, 241
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No: hu00416615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                            APPLICANT:
               APPLICANT:
                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                            94
                                                                                                                                                                                                                         61 AAATCCCACTTGAACCAACTGAAGAAAAAA 90
                                                                                                                                                                                                                                                          34
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                        1. TGTGACCTCTGTGATCGAATCATCATTGGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
                                                                                                                                                                                                                                                          90;
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Stuve, Laura L
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                                                                                                            Application US/60044082
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Ito, Laura Y.
Akerblom, Ingrid E.
Delegeane, Angelo M.
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                                              Stuve, Laura L.
Stuart, Susan G.
                                                                            Gooding, Douglas
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100.0%; Pred. No.
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Pred. No.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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Gapop 10.0 , Gapext 1
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'cgn2_6/ptodata/1/pna/US084_COMB.seq:*
'cgn2_6/ptodata/1/pna/US085_COMB.seq:*
'cgn2_6/ptodata/1/pna/US085_COMB.seq:*
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'cgn2_6/ptodata/1/pna/US108_COMB.seq:*
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/ptodata/1/pna/US081_COMB.seq:*
/ptodata/1/pna/US082_COMB.seq:*
/ptodata/1/pna/US083_COMB.seq:*
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8512.654 Million cell updates/sec
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Match
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Database

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: /cgn2_6/ptodata/1/pna/USB011_COMB.seq:*
: /cgn2_6/ptodata/1/pna/USB011_COMB.seq:*
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: /cgn2_6/ptodata/1/pna/USB013_COMB.seq:*
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!: /cgn2_6/ptodata/1/pna/USB018_COMB.seq:*
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

SUMMARIES

#### US-09-056-942-268 US-09-532-315-9510 US-60-044-082-268 US-09-532-315-9519 US-09-489-036-7332 US-09-948-138-7332 US-09-9515-128-21383 US-09-9515-128-21383 US-09-959-922-3465 US-09-959-922-3465 US-09-959-922-3465 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-9898-8888-8140 US-09-757-028-874 US-09-757-028-874 US-09-757-258-6006 US-09-705-2568-6006 US-09-705-2568-6006 US-09-1898-8886-11692 Description Sequence 1268, App 2610, Ap 2610, Ap 27319, Ap 27312, Ap 27332, Ap 2732, Ap 2732, Ap 2732, Ap 2732, Ap

B 5

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1271 AAATCCCACTTGAACCAACTGAAGAAAAGA 1300

AAATCCCACTTGAACCAACTGAAGAAAAGA 90

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; LOCATION: (191)..(1426)
US-10-380-731-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 119
LENGTH: 2130
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 90; Conserv
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                                                                                                                                        PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
PRIOR FILING DATE: 1993-08-03
PRIOR APPLICATION NUMBER: 09/008,119
PRIOR FILING DATE: 1998-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 9504, Application US/09532315B ENERAL INFORMATION:
                                                                                                                                                                                                                                                             URRENT APPLICATION NUMBER: US/09/532,315B

CURRENT FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: 07/916,491

RRIOR FILING DATE: 1992-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-09 NUMBER OF SEQ ID NOS: 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 21272-114
CURRENT APPLICATION NUMBER: US/10/380,731
CURRENT FILING DATE: 2003-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                                                                                                                                           PPLICANT: Mullahy, Sara J.

PPLICANT: Naughton, Rebecca E.

ITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING TRANSFERASES

ILLE REFERENCE: PD-1002 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Hyseq, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1271 AAATCCCACTTGAACCAACTGAAGAAAAGA 1300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                           APPLICATION NUMBER:
                                                                                                                     APPLICATION NUMBER: 08/196,364
                                     APPLICATION NUMBER: 08/438,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATCCCACTTGAACCAACTGAAGAAAAGA 90
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                    1995-05-10
                                                        1994-07-28
                                                                                                  1994-02-14
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08/179,873
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Pred. No. 1.8e-22;
Mismatches 0;
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Search completed: April 21, Job time: 52.7649 secs
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SOFTWARE: PERL Program
SEQ ID NO 9504
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 08/504,732 PRIOR FILING DATE: 1995-07-20
                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
LOCATION: 107, 113, 120-121
OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 287
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               emaining Prior Application data removed -
                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                        238 CAAATCCCACTTGAACCAACTNAAGGAAAG 267
                                                                                                                                                  178 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGGAATGGGCAGCGCACATAAAATC 237
                                                                                                              60 CANATCCCACTTGAACCAACTGAAGAAAAG 89
                                                                                                                                                                        1 TGTGACCTCTGTGATCGAATCATTGGGGATCGC-GAATGGGCAGCGCACATAAAATC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/137,951 FILING DATE: 1993-10-14
                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                            120-121, 174, 259, 279, 282
m, t, c, g, or other
                                                                                                                                                                                                                                                83.8%;
96.7%;
                  2003, 18:41:28
                                                                                                                                                                                                                                                                                                                                                                                                        ID No: hu00221292
                                                                                                                                                                                                                            Score 75.4; DB 6;
Pred. No. 2.3e-17;
0; Mismatches 2
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                                                                                                                                                                                                                                                                Length 287;
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RESULT 11
US-60-453-135-275
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; ORGANISM: Homo sapiens
US-60-453-135-275
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LENGTH: 2119
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 40554, Application:
Sequence 40554, Application:
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
APPLICANT: VENTER, J. SUCH AS NUCLEIC ACID ARRAYS, COMP
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION
                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 275
LENGTH: 2119
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 275, Application US/60453135
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                                                                                                          Best Local Similarity Matches 90; Conserv
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                             PENERAL INFORMATION:

APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: HUMAN
                                     1213
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                                                                       1 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
 AAATCCCACTTGAACCAACTGAAGAAAGA 90
                                     TGTGACCTCTGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 1272
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                                                                                                            Conservative
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100.0%; Pred. No.
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Pred. No. 1.
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Pred. No. 1.8e-22;
                                                                                                            Mismatches
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                                                                                                                             1.8e-22;
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                                     Matches
                                                        Best
                                                                       Query Match
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                                                                                                                                                                                                  TYPE: DNA
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                                                      Local
1 TGTGACCTCTGTGATCGATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
                                   l Similarity
90; Conserv
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NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 275
LENGTH: 2119
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-050-275
                                                               ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (191)..(1426)
US-09-659-671A-134
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                                                                                                                                                                              SOFTWARE: pt_FL_genes
SEQ ID NO 134
LENGTH: 2130
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: STENOSIS, METHODS OF
FILE REFERENCE: CL001457
                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/659,671A
CURRENT FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/453,050 CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                               FILE REFERENCE: 794
                                                                                                                                                                                                                                                                                                               APPLICANT: Wehrman, Tom
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Wovel Nucleic
TITLE OF INVENTION: Polypeptides
                                                                                                                                      ORGANISM: Homo sapiens
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Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                          Yang, Yonghong
                                                                                                                                                                                                                                                                                                                                                                                                            Ren, Feiyan
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                        Version 2.0
100.0%;
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       Score 90;
Pred. No.
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Pred. No. 1.8e-22
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                       Length 2130;
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FILE REFERENCE: CL001456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 274
SEQ ID NO 274
LENGTH: 1719
TYPE: DNA
ORGANISM: Homo sapiens
US-60-453-135-274
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 1271
; TYPE: DNA
; ORGANIZSM: Homo sapiens
US-60-453-050-276
                                                                                                                                                                                                                                                                                               US-60-453-135-274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: HUMAN
US-10-170-235-41123
                                                                                                                                                                                                                                                           Sequence 274, Application US/60453135 GENERAL INFORMATION:
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EQ ID NO 41123
LENGTH: 1719
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CURRENT FILING DATE: 2003-03-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig
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                                                                                                                                                                                                                       APPLICANT: CARGILL, Michele APPLICANT: IAKOUBOVA, Olga
                                                                                                                                                                                 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                813
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                                                                                                                                                                                                                                                                                                                                                                                                        61 AAATCCCACTTGAACCAACTGAAGAAAGA 90
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TRANSCRIPTS,
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Pred. No. 1.7e-22;
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Pred. No. 1.6e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEIC ACID ARRAYS, COMFOR DETECTING EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                     METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1719;
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FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15

60/298,918 6-18 60/380,710 INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

APPLICANT

Van 't Veer, Laura Johanna Van de Vijver, Marc J.

Roberts, Christopher J.

LICANT

Bernards,

PPLICANT

PRIOR APPLICATION NUMBER: 10/PRIOR FILING DATE: 2002-06-14

OF SEQ ID NOS:

ID NO 1692

ORGANISM: Homo sapiens

PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2001-06-18 PRIOR APPLICATION NUMBER: 60/ PRIOR FILING DATE: 2002-05-14

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US-60-453-050-274
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Best Local Similarity
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Best Local
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TYPE: DNA
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EQ ID NO 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8276
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CURRENT FILING DATE: 2003-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele APPLICANT: LUKE, May
                                                                                     10-342-887-1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH ITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND UILE REFERENCE: CL001457
   PPLICANT:
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                                                                                                                                                                                                                        813 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAAATCC 872
                                                                                                                                                        873 AAATCCCACTTGAACCAACTGAAGAAAAGA 902
                                                                                                                                                                                       61 AAATCCCACTTGAACCAACTGAAGAAAGA 90
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                                                                  1692, Application US/10342887
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                               Dai, Hongyue
                   He, Yudong
Linsley, Peter S
                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 1.7e-22;
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Pred. No. 1.
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1.7e-22;
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SEQ ID NO 9519
LENGTH: 289
TYPE: DNA
                                                                                                    Matches
                                                                                                                                 Query Match
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CURRENT FILING DATE: 2000-03-24
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                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1993-10-14
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APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00815059
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                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1994-01-
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LOCATION: 228, 241
OTHER INFORMATION:
                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                  84
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61 AMATCCCACTTGAACCAACTGAAGAAAAGA 90
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                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/137,951
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/504,732
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                                                              TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
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                              TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 143
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                                                                                                  Conservative
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7-17
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                                                                                                            Score 90; DB 6;
Pred. No. 1.1e-22;
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Pred. No. 1.1e-22;
; Mismatches 0;
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                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                            See File Wrapper or PALM.
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RESULT 5
US-60-453-050-276
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                                                  Sequence 276, Application US/60453050 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT FILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 41124
LENGTH: 1271
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DET FILE REFERENCE: CLOO1456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT APPLICATION NUMBER: 05/60/453,135
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Best Local 9
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                APPLICANT: CARGILL, Michele APPLICANT: LUKE, May
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TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HU
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 12
TYPE: DNA
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ITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
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                                                                                                                                                            425 AAATCCCACTTGAACCAACTGAAGAAAAGA
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Pred. No. 1.6e-22;
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Pred. No. 1.6e-22;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Sequence:
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US-9-659-671A-134

US-10-380-731-119

US-9-532-3158-9504

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Sequence 1692, Ap
Sequence 275, App
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Sequence 275, App
Sequence 219, Ap
Sequence 219, Ap
Sequence 2119, Ap
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Sequence 2119, Ap
Sequence 2512, Ap
Sequence 254990, A
Sequence 25285, A
Sequence 9512, Ap
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Sequence 65757, A	Sequence 9517, Ap	Sequence 16177, A	Sequence 1231, Ap	Sequence 1231, Ap	Sequence 45678, A	Sequence 21447, A	Sequence 5708, Ap	Sequence 16297, A	Sequence 162940,	Sequence 136, App	Sequence 136, App	Sequence 745, App	Sequence 746, App	Sequence 681, App	Sequence 53708, A	Sequence 54885, A	Sequence 35887, A	Sequence 52531, A	Sequence 18601, A	Sequence 80102, A	Sequence 36790, A	Sequence 66580, A

### ALIGNMENTS

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SOFTWARE: PERL Pro
SEQ ID NO 9510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 07/916 491
PRIOR FILING DATE: 1992-07-17
PRIOR APPLICATION NUMBER: 07/977,780
PRIOR FILING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 08/100,523
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PRIOR FILING DATE: 1994-01-11
PRIOR APPLICATION NUMBER: 08/504,732
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APPLICANT: Delegeane, Angelo M.
                                                                                                                                                                                                                  PRIOR FILING DATE: 1993-10-14
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00416615
                                        ORGANISM: Homo sapiens FEATURE:
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APPLICATION NUMBER: 08/438,571
FILING DATE: 1995-05-10
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APPLICATION NUMBER: 09/008,119
FILING DATE: 1998-01-16
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APPLICATION NUMBER: 08/282,991
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  261
                                                                         241 CysValGlyTyrArgGlnMetTrpGluTyrLeuGlnGlyAspTyrAlaTyrGluGluMet
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IlePheArgGlyIleCys---
                    ATCACTGAGGGAAAATGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAA 937
                                                                                                                                                       Arg---GlyAspLeuAsnIleAsnLeuProSer-------IleArg 240
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|ThrGluGluLysGlyGluAlaLeu-----ProTyrAspPhe 190
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Search completed: April 21, Job time: 56.8883 secs

2003, 18:51:09

Qy 143 CAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGAAGGCCTAGAC 202       :::::	Appothetical protein F2ZK18.150 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999 C:Accession: T05569 R:Bevan, M: Wedler, H: Wedler, E: Wambutt, R.; Hoheisel, J:: Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999 A;Reference number: 215419 A;Residues: 1-318 <bev> A;Residues: 1-318 <bev> A;Residues: 1-318 <bev> A;Cross=references: EMBL.AL035356 A;Experimental source: cultivar Columbia; BAC clone F2ZK18 C:Genetics: A;Map position: 4 A;Note: F2ZK18.150 C;Superfamily: delta(2)-isopentenylpyrophosphate transferase Alignment Scores: A;Apap position: 4 A;Note: F2ZK18.150 C;Superfamily: delta(2)-isopentenylpyrophosphate transferase Alignment Scores: 1.08e-18 Fred. No.: 338.00 Percent Similarity: 42.23% Best Local Similarity: 26.43% Ouery Match: 97 Percent Similarity: 26.43% Ouery Match: 98 Best Local Similarity: 26.43% Ouery Match: 98 CTGTAGTGTATTCTCGGGGCCACGGGCAAATCCACGGTGGGGTTGCAGCTAGGC 142 US-09-513-151-3 (1-2041) x T05569 (1-318)  Ouery Match: 10 Db 7 MetValvalliewerGlvAiathrGlvGarGGAAATCCACGGTGGGGTTGCAGCTAGGC 142  11</bev></bev></bev>	Qy 794 CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA 853    :::    :::	Qy 614 TTTCTCCCATCGTCAACATACGGAAGAAGGTGGTGGTCGTCTGGAAGTTC 673
RESULT 15.  RESULT 15.  F64046  F64046  Gelta(2)-isopentenylpyrophosphate transferase (EC 2.5.1) - Haemophilus influenzae delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1) - Haemophilus influenzae C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999 C; Accession: F64046  R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavav; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidm; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.I science 269, 496-512, 1995  A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vent A;Tille: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Status: nucleic acid sequence not shown; translation not shown  A;Residues: F64046  A;Status: nucleic acid sequence not shown; translation not shown  A;Rolecule type: DNA  A;Residues: 1-311 <tigr>  A;Cross-references: GB:U32692; GB:L42023; NID:g1573013; PIDN:AAC21746.1; PID:g15730: C;Superfamily: delta(2)-isopentenylpyrophosphate transferase C;Keywords: nucleotidyltransferase; tRNA modification</tigr>	Db 159 AspLeuMetMetLysSerGlyMetPheGluGluIleAlaGluPheHiSArg	Qy 623 CGTCAACATACGGAAGAAGGTGGTGGTGCCCTTGGAAGGTCCTCTGAAGTTCTCTAACCCT 682	Qy 443 GAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAA 502  Db 114

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C;Genetics:
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C;Date: 10.May-2001 #sequence_revision 10.May-2001 #text_change 22-Oct-2001
C;Accession: B89905
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimi C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
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A; Cross-references: GB:BA000018; PID:g13701103;
A; Experimental source: strain N315
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                                                                       AAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGA-----ATCTCTCATAGTGAA
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                             ArgValLeuArgAlaIleGluTyrTyrLeuLysThrLysLysLeuLeuSerAsnArgLys
                                                                                                                                                                                                                                                                                                             TyrIleGlnSerLeuIleTyrAsnTyrGluLeuGluAspGluThrValThrProAlaGln
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                                                                                                                        AspTyrLeuAlaGlnPheAspAlaValSerAlaGluAsnIleHisProAsnAsnArgGln
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PIDN:BAB42398.1; GSPDB:GN00149

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A;Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72366
A;Status: preliminar...
                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001728; GB:AE000512; A;Experimental source: strain MSB8 C;Genetics: C;Gene: TM0525 A;Gene: TM0525 C;Superfamily: delta(2)-isopentenylpyrophospha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tRNA delta-2-isopentenylpyrophosphate transferase - Thermotoga maritima (strain MSB8) C;Species: Thermotoga maritima (c;Species: Thermotoga maritima C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000 C;Accession: C72366
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Higgarrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <ARN>
                                                                                                                                                                         Percent Similarity:
Best Local Similari
                                                                                        US-09-513-151-3 (1-2041) x C72366 (1-305)
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Matches:
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A;Title: Genome sequence of an obligate intracellular pathogen of A;Reference number: A71570; MUID:99000809; PMID:9784136 A;Recession: A71473 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-339 <ARN-A;Cross-references: GB:AE001349; GB:AE001273; NID:g3329226; PIDN:AA;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                                              probable tRNA pyrophosphate transferase - Chlamydia trachomatis (serotype D, C;Species: Chlamydia trachomatis C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999 C;Accession: A71473 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L Science 282, 754-759, 1998
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                                                                                                                                               humans: Chlamydia
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AC1599
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001
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A;Experimental source: strain Clipl1262
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A; Residues: 1-305 <GLA>
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..; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; I
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GlnValHisHisThrLeuAsnGluAlaTyrGlnProLeu
                                                                                                                           TrpGlnMetLeuAspGlnLeuAspProLysSerAlaGluLeuIleHisGluAsnAsnLys 156
                                                                                                                                                                                             AlaTyrArgArg------GluLeuAspGlnLeuAspLysThrThrLeu 136
                                                                                                                                                                                                                                                              GlyLeuTyrIleGlnSerValPheTyrAspTyrGlyPheGlyAsnAlaSerGluAspLys 122
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                                                                                                                                                                                                                                                                                                                              ArgGlyLeuIleGluSerIleHisAsnArgGlyLysLeuProIleIleValGlyGlyThr 102
                                                                                                                                                                                                                                                                                                                                                              ACTGCTCTGATTGAAGATATATTTGCCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACC 376
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                                CTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCT 676
                                                                                              CGCANAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTT 616
                                                                                                                                                              CACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATGACAAA 556
                                                                                                                                                                                                                               GGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTT 496
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                                                                 ArgArgValIleArgAlaLeuGluValIleHisLeuThrGlyLysProPheSerGluTyr
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A;Molecule type: DNA
A;Residues: 1-309 <KUR>
A;Cross-references: GB:AE001437; PIDN:AAK79799.1;
A;Experimental source: Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solve A; Reference number: A96900; MUID:21359325; PMID:21359325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CAC1835
C; Superfamily: delta(2)-isopentenylpyrophosphate
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                                              AlaIleAspAspIleThrSerArgLysLysTyrProIleIleValGlyGlyThrGlyLeu 102
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  TACATTGAATCTCTGCTCTGGAAAGTT---CTTGTCAATACCAAGCCCCCAGGAGATGGGC
                                                                                                                                                ValValAspPro···SerGluGluPheSerValAlaSerPheLysLysMetAlaGlnAsn
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                                                                                                 CTGATTGAAGATATTTGCCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTAT
                                                                                                                                                                                                                                               {\tt IleGlySerAlaLysValThrLysGluGluMetLysGlyIleLysHisHisLeuIleAsp}
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378.50
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.;
A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.;
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AF1236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-305 <GLA>
A;Cross-references: GB:NC_003210; PIDN:CAC99372.1; PID:g16410710; GSPD
A;Genetics:
A;Gene: miaA
                                                                                                                                                                                                                                                                     tRNA isopentenylpyrophosphate transferase homolog miaA [imported] - Listeria C;Species: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AF1236
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Muccleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83945
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A;Residues: 1-314 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06085.1;
A;Experimental source: strain C-125
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                          608 AGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTG
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                                                                         AsnAsnTyrArgArgVallleArgAlaLeuGluIleIleLysLeuThrGlyLysThrVal 176
                                                                                                                        CATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCAT
                                                                                                                                                                      GlnAlaLeuHisAspLysLeuSerLysIleAspProLysAlaAlaAlaAlaIleHisPro
                                                                                                                                                                                                                                                                                                             ACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAA-----AAGGAGGATGGTCTT 490
                                                                                                                                                                                                                                                                                                                                                                                                          TACATTGAATCTCTGCTCTGGAAAGTT----CTTGTCAATACCAAGCCCCAGGAGATGGGC 439
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                                                                                                                                                                                                                                                                                                                                                           TyrValAsnAlaValIleHisGlnPheAsnLeuGlyAspIleArgAlaAspGlu-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuIleThrGluIleHisGluArgGlyArgLeuProPheLeuValGlyGlyThrGlyLeu 103
                                                                                                                                                                                                                                                                 ----AspTyrArgHisGluLeuGluAlaPheValAsnSerTyrGlyVal
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C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.,
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardin
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; May,
M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scan
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sekeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshic
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: G6957
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C;Superfamily: delta(2)-isopentenylpyrophosphate
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A; Residues: 1-314 <KUN>
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A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                             No.:
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    200 GACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATC
                                                   27 AlaLysSerLeuAsnAlaGluIleIleSerGlyAspSerMetGlnIleTyrLysGlyMet
                                                                                                                                                                                            80 CCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTA
                                                                                                                                           ProValValIleLeuValGlyProThrAlaValGlyLysThrAsnLeuSerIleGlnLeu
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                                                                                                  GGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTATGAAGGCCTA 199
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305 AGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCCGAGACAAAATTCCTATTGTT 364	245 CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC 304	185 GTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGGCAGAGAAATCTGC 244 :::             ::::	125 CTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAG 184       :::        21 LeuAlavalAspLeuAlaSerHisDheProValGluIleIleAsnAlaAspAlaMetGln 40	65 CTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGGCACGGGGCACGGGCAAATCCACG 124 :::::::: 1	76 (1-461)	Best Local Similarity: 26.67% Mismatches: 137 Query Match: 13.17% Indels: 108 DB: 2 Gaps: 17	3.2e-29 Length: 471.00 Matches: 48.96% Conservative:	Gene: At2g27760 Map position: 2	A; Molecule type: DNA A; Residues: 1-461 <sto> A; Cross-references: GB:AE002093; NID:g3860256; PIDN:AAC73024.1; GSPDB:GN00139 C; GenetLcs:</sto>	lysis of chromosome 2 of the plant Arabidor 0; MUID:20083487; PMID:10617197	R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999	hypothetical protein At2g27760 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F84676	SULT 5	1235 AAC 1237 	1193ARCCHACTGAAGAAAGAAGAAGAATTGGACTCAGATGCTGTC 1234 :::            ::: 446 ThrThrArgHisLysAsnSerGinThrTyrLysAsnArgGluValGlnGluAlaGluVal 465		408SerIleGluArgAspLeuTrpThrGlnTyrValCysGluAlaCysGlyAsnLys 425	CCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTCTGTGTGACCTCTGTGATCGA	1037 AGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCAATAAAGATG 1081    :::::           ::: 391 CysPheLeuGluThrGluThrGluSerGlyArgAspProThrSerGlyLys 407	989TCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAATCGTGCAA 1036
oy	Db Q	Db 49	dd 40	D 0 9	, Dp	Qy	Оу	Оу	ОУ	о Оу	Qу	Оу	B 8	o d	ργ	, 0y g	D Oy	da 	o p	рь Qy
1142 ATCATTGGGGATCGCGAATGGGCAGCACATAAAATCCCAAATCCCACTTG 1192 :::                  ::: :::::   422 LeuArgGlyArgHisGluTrpGluHisHisLysGlnGlyArgThrHisArgLysArgThr 441	IRCANICANGCICAGANCAAGANGAAGITAICACCIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGACCICIGIGIGIG		LysSerGluGluSerTrpAsnAlaGlnValValLysProAlaSerGluIleIleArgCys	933 GTCCCCCTGTCTATGGCTTAGGGTATTGGTTTTTGAAGCTCTCTTTTGAAGTTTTTGAAGTTTTTTGAAGTTTTTTGAAGTTTTTT	AspArgValLysLeuAsnThrArgArgLeuLeuArgArgGlnLysArgArgValSerArg		944 GGTCCCATT	896GAAAATGCACACTGGAGACTAGTAACCAGCTTCTAAAGAAAGGACCT 943	845 ATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAG 895 :::           :::     :::::   267 LeuargGlnSerIleGlyValargGluPheGluAspPheLeuLysIleHisLeuSerGlu 286	785 TTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGT 844 	725 CGCTTGGATAAGAGGTGGATGACATGCTTGCTGCTGGCTCTTGGAGGAACTAAGAGAT 784 	665 CTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAG 724	AlaGluValAspSerPhePheLeuThrSerArgGlnAsnTrpGlyCysIleAsnAlaSer	178 TyrLeuSerLeuHisAlaSerArgGlyValLeuProSerLystLeuTyrGlnGlyLysThr 197	158 GluLeuAspProValAlaAlaAsnArglieHisProAsnAsnHisArgLysIleAsnGin 1// 572 AGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTTCTCCCATCGTCAACAT 631	CAGGTGGACCCAGAAATGGCTGCCAAGCTGCCATCCACATGACAAACGCAAAGTGGCCAGG :::::::	464 GTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAAACGCCTAAGC 511 ::::::    ::::::    :::::::    ::::::::		100 ValGlyGlyThrHisTyrTyrIleGlnAlaValValSerLysPheLeuLeuAspAspAla 119 425 CCCCAGGAGATGGGCACTGAGAAA	80 ArgaspPheThrValProLeuIleGluGluIleValSerArgAsnHisIleProValLeu 99 365 GTGGGAACCAATTATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAG 424

Alignment Scores: 5.72e-31 Length: 466 Prod. No.: 493.00 Matches: 133 Score: 493.00 Conservative: 108 Best Local Similarity: 50.10% Mismatches: 138 Query Match: 13.79% Indels: 102 DB: US-09-513-151-3 (1-2041) x T52061 (1-466)  Qy 41 CCTGTGGGCAGTGGGCTCAGGGGCCTGCAACGGACCCTACCTCTTGTAGTGATT 94		1031 GTGCAAAGTTTCATCCAAGGCCACAAGACCTCCAATAAAGATGCCATACAAT 1   1   1   1   1   1   1   1   1   1	824AGCCAGGACTATCAACATGGTATCTTCCAATC.	Db 210 AspSerLeuValLeuMetProArgLeuAspLysArgValAspLysMetLeuSerHisGly 229  Qy 764 CTCTTGGAGGAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAAT 823     :::::  :::   bb 230 LeuValAspGluIleLysSerMetLysSerLeuAlaGluSer 243
Qy       941 CCTGGTCCCATT       952         Db       311 LeuArgLySIleLeuAsnPheProLysAspAspLysLeuArgIleMetLeuGluGluAla 330         Qy       952	Qy 722 GAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGTGGTCTTGGAGAACTAAGA 781  Qy 722 GAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCTGGTGGAGGAACTAAGA 781	143 AlaAspvalAlaSerValValAspGlnAspMetValValGluSerValPheGlyArgAsp 482 GATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTG	46 215 66 275 275 86 86 335 105 395	Qy 95 CTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGC 154

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RESULT 3
                                                      411 GlnLysHisIleAspGlyLysLysHisLysHisHisAlaLysGlnLysLys
                                                                                                                                                                                                                                                                               372 IleAspLeuPheGluAspIleSerThrAspThrAsn---ProIleLeuLysGlySerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GluGluArgLeuAspGlyArgValAspLysMetIleLysLeuGlyLeuLysAsnGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 IleSerAsnGlnGluLeuTrpAspGluLeuLysLysIleAspGluLysSerAlaLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 AspValAspSerLysSerArgThrSerSerGluSerSerGluAspThrGluGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 ThrTyrTyrAlaGluSerValLeuTyrGluAsnAsnLeuIleGluThrAsnThrSerAsp
                                                                                                          GCAGCGCACATAAAATCCCAATCCCACTTGAACCAACTGAAGAAAAGAAGA 1213
                                                                                                                                                                 AlaAsnIleLeuLeuAsnCysGluIleCysAsnIleSerMetThrGlyLysAspAsnTrp
                                                                                                                                                                                                                        AAGAGAAGTTATCACCTGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGG
                                                                                                                                                                                                                                                                                                                                                                                          ----LysTyrArgIleIleSerAspGlyMetAspIleValAspGlnTrpMetAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgSerAspGlyAspArgLysMetAlaSerThrLysMetLeuAspThrSerAsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGGACCTGGTCCC---ATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGAGACT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerGluArgAspThrLeuAsnGlyAspLysLeuPheLysGlnGlyCysAspAspValLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrGlyValMetGlnCysIleGlyLeuLysGluPheValProTrpLeuAsnLeuAspPro 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGluPhe-----TyrAsnGluHis-----AlaGluTyrIleAsnHisSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGGGGCTCTTGGAGGAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyArgLeuArgPheAspAsnSerLeuValIlePheMetAspAlaThrProGluValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleArgLysSerGluLeuValGluLysGlnLysSerAspGlu---ThrValAspLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuHisProAsnAsnArgTyrArgValGlnArgAlaLeuGlnIlePheArgGluThrGly
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C;Species: Schlzosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T38664
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-434 <MUR>
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GARATGGCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgValIleAspGluIleHisSerGlnGlyLysIleProIleValValGlyGlyThrHis
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                                                                       GGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCT
                                                                                                          TyrPheHisThrGlyArgProProSerGluIleTyrSerGluGlnLysMetLysSerSer
                                                                                                                                               TTTGAAGAAACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGT
                                                                                                                                                                                    ValMetAlaGluGlnTrpHisProArgAspThrArgLysIleArgArgSerLeuGluIle
                                                                                                                                                                                                                                                                                                GTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCA
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                                    ·GlySerLysLeuArgTyrLysSer---LeuIlePheTrpAlaPheAla
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Title:
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-Q-/cgn2_1/USPTO_spool/US99513151/runat_15042003_141144_26390/app_query.fasta_1.2446
-Q-/cgn2_1/USPTO_spool/US99513151/runat_15042003_141144_26390/app_query.fasta_1.2446
-DB-PIR_73 -QFMT-fastan -SUFFIX-m2p.rpr -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -THLEN-0 -MAXLEN-200000000
-USER-US09513151_@CGN_1_1_58 @runat_15042003_141144_26390 -NOPU-6 -ICPU-3
-USER-US09513151_@CGN_1_1_58 @runat_15042003_141144_26390 -NOPU-6 -TGAPEXT-7
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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## ALIGNMENTS

R;Najarian, D.; Dihanich, M.E.; Martin, N.C.; HUPPEL, A.M. Rol. Cell. Biol. 7, 185-191, 1987
A;Title: DNA sequence and transcript mapping of MOD5: féatures A;Reference number: A26717; MUID:87172703; PMID:3031457
A;Accession: A26717 A:Cross-references: MIPS:YOR274W; SGD:S0005800 A;Map position: 15R C;Keywords: transferase A; Molecule type: DNA
A; Residues: 1-428 <CHW>
A; Cross-references: EMBl N;Alternate names: protein 05447w; prot C;Species: Saccharomyces cerevisiae C;Date: 12-Jul-1996 #sequence_revision C;Accession: S67176; A26717; S72045 R;Cheret, G.; Sor, F A;Title: DNA sequence analysis of the VPH1-SNF2 region on A;Reference number: S72039; MUID:97051594; PMID:8896271 A;Accession: S72045 A; Reference number: A; Accession: S67176 submitted to the Protein Sequence Database, A; Reference number: S67169 C; Genetics: R;Cheret, G.; Bernardi, A Yeast 12, 1059-1064, 1996 A;Cross-references: EMBL:M15991
R;Cheret, G.; Bernardi, A.; Sor, F. A; Molecule type: DNA A; Residues: 1-374, 'R', 376-428 <NAJ> A; Experimental source: strain S288C A; Gene: SGD: MOD5 A; Note: the nucleotide A; Status: nucleic A;Cross-references: EMBL:Z75182; NID:g1420613; PID:e252418; A; Residues: 1-428 <CHE> A; Molecule type: tRNA isopentenyltransferase (EC 2.5.1.8) -DNA acid sequence not shown; translation not shown EMBL:X89633; NID:g1279694; PIDN:CAA61780.1; PID:g1419759 ide sequence was submitted to the EMBL Data Library, June E.; Martin, N.C.; Hopper, A.K. 1987 protein 12-Jul-1996 #text_change 21-Jul-2000 yeast (Saccharomyces YOR274w July 1996 chromosome PID:g1420614; of the cerevisiae) ž 5' region whic of. MIPS:YOR27 Saccharom 1995

SUMMARIES

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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#### RESULT 1 ABB97295 Novel human protein SEQ ID NO: 27-JUN-2002 (first entry) ABB97295; ABB97295 standard; Protein; 411 AA ALIGNMENTS

Human; antianemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST; expressed sequence tag.

Homo sapiens

WO200222660-A2

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.

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17-NOV-2000;
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-239937P. -240960P. -241221P.

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                                                                                                                                                                                          The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence
                                                                                                                                                                                                                                                         Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition -
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2000US-0225213.
2000US-0225214.
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2000US-0229509

2000US-0229513

2000US-0230438 2000US-0231242

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The present invention relates to the isolation of novel human enzyme copypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences concoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyses, isomerases or ligases. The sequences of the invention are useful in the clisomerases or ligases. The sequences of the invention are useful in the clisomerases including hyperproliferative disorders (e.g. cancer), communodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. carcin), cc (e.g. arthritis), neurological disorders (e.g. Alzheimer s disease), cometabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), cometabolic disorders (e.g. henylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. affilmanza). The polynucleotides of the invention can also be used in gene therapy.

AAUZ2915-AAUZ3814 represent the novel human enzyme polypeptides of the
                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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05-DEC-2000;
                         invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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N-PSDB; AAS41268.
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2000US-0249265.
2000US-0249297.
2000US-0249299.
2000US-0249300.
2000US-0250160.
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2000US-0251868.
2000US-0251869.
2000US-0251989.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0249213.
2000US-0249214.
2000US-0249215.
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2000US-0249209.
2000US-0249210.
2000US-0249211.
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21-SEP-2000; 25-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232401. 2000US-0233063. 2000US-0233064. 2000US-0233065. 14-SEP-2000;

2000US-0231968. 2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232400.

2000US-0232080 2000US-0232081

20-OCT-2000 20-OCT-2000 20-OCT-2000 20-OCT-2000 01-NOV-2000 08-NOV-2000 08-NOV-2000

2000US-0246523. 2000US-0246524. 2000US-0246525.

2000US-0246478

13-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000;

2000US-0241221. 2000US-0241785. 2000US-0241786.

2000US-0239935. 2000US-0239937. 2000US-0240960.

2000US-0237038 2000US-0237039 2000US-0236367

-0236370

2000US-0241787. 2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

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Query Match:
DB:
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                                                         03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                     Penn
      WPI; 2001-496933/54
                                   (MOLE-)
                                                                              26-MAY-2000;
30-JUN-2000;
                                                                                             04-FEB-2000;
                                                                                                            30-JAN-2001; 2001WO-US00662
                                                                                                                            09-AUG-2001
                                                                                                                                          WO200157271-A2
                                                                                                                                                        Homo sapiens
                                                                                                                                                                       disease;
                                                                                                                                                                              Human; microarray; single exon probe; gene expression; breast
                                                                                                                                                                                            Peptide #1530 encoded by breast cell single exon nucleic acid
                                                                                                                                                                                                              01-FEB-2002
                                                                                                                                                                                                                             ABB28879;
                                                                                                                                                                                                                                         ABB28879 standard;
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                    SG,
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                                                                                                                                                                                                                                                                                                    PheArgAsnArgAlaThrAlaLeuIleGluAspIlePheAlaArgAspLysIleProIle
                                   MOLECULAR DYNAMICS INC
                    Hanzel
                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-06323687.
2000US-0236359.
                                                                                                                                                                                                            (first entry)
                                                 2000GB-0024263.
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                    DK,
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123.00
100.00%
100.00%
18.61%
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                   Chen
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                    Rank DR
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Indels:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater. diversity of probes for measuring gene expression, with far less blas than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                        30-JAN-2001;
                                                                                        09-AUG-2001.
                                                                                                                       WO200157277-A2
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                   Human; foetal
                                                                                                                                                                                                                Peptide #1561
                                                                                                                                                                                                                                                                               ABB34055;
                                                                                                                                                                                                                                                                                                           ABB34055 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC
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                                                          2001WO-US00669
                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                               encoded by human foetal liver single exon probe
                                                                                                                                                                                liver; gene expression;
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48.00
100.00%
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7.26%
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04-FEB-2000; 26-MAY-2000; 30-JUN-2000;

2000US-0180312. 2000US-0207456. 2000US-0608408.

nucleic English

acid

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Best Local Si
Query Match:
DB:
RRESULT 7
AAMS4847
ID AAMS4837
XX - AAMS4
AC AAMS2
XX DS -N
DT 05 -N
XX Huma
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this pattent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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04-FEB-2000; 2000US-0180312
                             30-JAN-2001;
                                                                                          WO200157275-A2
                                                                                                                           Homo sapiens
                                                                                                                                                                      microarray; Alzheimer's
                                                                                                                                                                                        Human; brain expressed
                                                                                                                                                                                                                        Human brain
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                                                                                                                                                                                                                                                                                                                    AAM54837 standard;
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                                                                                                                                                           cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AA;
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2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                    expressed single
                               2001WO-US00667
                                                                                                                                                                                                                                                    (first entry)
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48.00
100.00%
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7.26%
22
                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                                        exon;
                                                                                                                                                                        disease;
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                                                                                                                                                                      gene expression analysis; probe;
ase; multiple sclerosis; schizophrenia;
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Matches:
Conservative:
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AAM67220
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Best Local Similarity:
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2000;
04-OCT-2000;
                                                                                                                                          Homo
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brains -
04-FEB-2000;
26-MAY-2000;
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                                              30-JAN-2001;
                                                                           09-AUG-2001
                                                                                                           WO200157276-A2
                                                                                                                                                                        microarray; cancer; leukaemia;
                                                                                                                                                                                       Human; bone marrow
                                                                                                                                                                                                                        Human
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                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgHisHisMetIleSerPheValAspProLeuValThrAsnTyrThrValValAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC
                                                                                                                                                                                                                        bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                        marrow
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-0024263.
2000US-0180312
2000US-0207456
                                            2001WO-US00668
                                                                                                                                                                                                                                                     (first entry)
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48.00
100.00%
100.00%
7.26%
                                                                                                                                                                                        expressed
                                                                                                                                                                                                                                                                                                                    Protein;
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                                                                                                                                                                        lymphoma; myeloma
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                      encoded protein
                                                                                                                                                                                        gene expression analysis; probe;
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ID NO:

27526.

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AAM15066
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                                                                                                                                                                                                                                                       RESULT 9
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to the improved expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
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                                                                                                                                                                                                               AAM15066
                                                   30-JAN-2001;
                                                                        09-AUG-2001
                                                                                             WO200157278-A2
                                                                                                                  Homo sapiens.
                                                                                                                                       cervical
                                                                                                                                               Probe; human; microarray; gene
                                                                                                                                                                     Peptide #1500
                                                                                                                                                                                          12-OCT-2001
                                                                                                                                                                                                                                  AAM15066 standard;
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                                                                                                                                                                                                                                                                                                                               CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC
                                                                                                                                                                                                                                                                                                                                                                                  GTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGC
                                                                                                                                                                                                                                                                                                                     ArgHisHisMetIleSerPheValAspProLeuValThrAsnTyrThrValValAspPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid
zing gene expression in human bone marrov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                    2001WO-US00670
                                                                                                                                                                                          (first entry)
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                                                                                                                                                                     encoded
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48.00
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                                                                                                                                                                     probe
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                                                                                                                                                expression; cervical
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Matches:
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                                                                                                                                                                     cervical gene expression
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0
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                                                                                                                                                epithelial cell;
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DB:
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                            genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                          09-AUG-2001
                                                                                                                       Probe;
                                                                                                                                            Peptide #1547 encoded by probe for measuring placental gene
                                                                                                                                                                                                               AAM27510 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                               WO200157272-A2
                                                                                      Homo sapiens
                                                                                                                                                                    17-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic acid probes useful zing gene expression in human cervical epithelial cells
                                                                                                           microarray;
c disorder.
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2000US-0236359.
2000GB-0024263.
                                                                                                                                                                 (first entry)
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48.00
100.00%
100.00%
7.26%
                                                                                                                      human;
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                                                                                                                       placenta;
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Matches:
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04-FEB-2000; 2000US-0180312 30-JAN-2001; 2001WO-US00663

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RESULT 11
AAY02534
ID AAY02534
AC AAY02
XX AFT 15-JU
XX PART1
XX GF0-1
KW HAD-1
KW Phys1
XX Phys1
XX Drosc
XX Drosc
XX W0991
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Best Local Similarity:
Query Match:
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Score:
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                            gro-1 operon; gro-1 gene; gop-1 gene;
hap-1 gene; cancer; aging; longevity;
physiological clock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn
          25-AUG-1997;
                                                   04-MAR-1999
                                                                      W09910482-AJ
                                                                                         Drosophila sp
                                                                                                                                                      Partial sequence of the Drosophila homologue of gro-1.
                                                                                                                                                                            15-JUL-1999
                                                                                                                                                                                                AAY02534;
                                                                                                                                                                                                                    AAY02534 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             No : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID No 27779; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                              20-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human genetic disorders.
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                                                                                                                                                                                                                                                                                                                                           SG,
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2000US-0608408.
2000US-06323667.
2000US-0234687.
2000US-0234685.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
         97CA-2210251
                              98WO-CA00803
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48.00
100.00%
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7.26%
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Matches:
                                                                                                                        gop-2 gene; gop-2 gene;
tumour formation;
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RESULT 12
AAG74967
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Best Local Similari
Query Match:
DE XXX PRR PRX TO XXX XXX DE XXX XXX DE XXX XXX DE XXX PR XX PR XXX PR X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and/or prognosis, useful for enhance
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                                                                         Ruben
                                                                                                                                                                             29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                            05-APR-2001
                                                                                                                                                                                                                                                                                                                                                               WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG74967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene, together with the gop-1, gop-2, gop-3 and hap-1 genes enables study of a physiological clock. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 10; 93pp; English.
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                                                                                                                                                                                                                                                        28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
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                                                                                                                         (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity:
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                                                                      Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 AA;
                                                                                                                                                                                                                                                        2000WO-US26524
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                                                                                                                         GENOME
                                                                                                                                                                             99US-0157137.
99US-0163280.
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                                                                         Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein SEQ
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Matches:
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WPI; 2001-235357/24 N-PSDB; AAH34372.

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US-09-513-151-3 (1-2041) x AAG74967 (1-94)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1017 CTGCTCTTGAAATCGTGCAAAGTTTCA 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 7257; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998
WPI; 1998-063077/06
                                                                                                            29-OCT-1996;
21-JUN-1996;
                                                                                                                                                                                                                                                                                                           stimulatory
                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor derived peptide 1168
                                                                                                                                                                                                                                                                                                                                                                                                                           AAW47911;
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                                                                                                                                                                                                                             W09748725-A1
                                                            (PEPT-) PEPTECH LTD.
                                                                                              06-SEP-1996;
                                                                                                                                                               20-JUN-1997;
                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                         tumour necrosis factor; neutrophil; monocyte; macro;
atory activity; immunosuppressant; cancer; infection
                              Rathjen DA,
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                                                                                           96AU-0003309.
96AU-0000610.
96AU-0002165.
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                              Sleigh JM,
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                                                                                                                                                                                                                                                                                                                            macrophage;
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Sequence

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versus host disease.

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Tumour necrosis factor derived peptide(s) having neutrophil and-or monocyte-macrophage stimulatory activity - used for treating e.g. infections, immunosuppression or cancers % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a peptide derived from a human tumour necrosis factor peptide. The peptide can have neutrophil and/or monocyte/macrophage stimulatory activity. The peptide is derived from the sequence of tumour necrosis factor (TNF) derived peptide 419 (PSTHYLITHTI; see AU/4762/91 and 44664/93). It can have improved properties such as increased potency, extended in vivo half life or, particularly, specificity of action. It can have neutrophil stimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS, cancer, diabetes, nosocomial infection, tuberculosis, cystic fibrosis, community acquired pneumonia, meningitis, Mycobacteria, Chlamydia, Brucellae, Francisella, Pasteurellosis, Legionellosis, Histoplasmosis, Listeriosis, Pneumocystis carnii, Trypanosoma cruzi, coccidian parasitical infection, an inherited primary neutropenic disorder, an inherited primary defect of phagocytic cell function, an acquired inherited secondary defect of phagocytic cell function, an acquired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 44; 65pp; English
                                                                                                                                                                                                                                                                                                 defect of phagocytic cell function, immunosuppression due to the administration of immunosuppressive drugs, and other bacterial, viral or protozoan infection, infectious mononucleosis, paroxyson nocturnal, haemoglobinuria, leukaemia, lymphoma, myelofibrosis, o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity (class 1), equal neutrophil and monocyte/macrophage stimulatory activity (class 2), or preferentially enhanced monocyte/macrophage stimulatory activity (class 3). It can be used for the treatment or prevention of infections. In particular, it can be used for treating
                                                                                                                                                                                                                                                                                                            lymphoma, myelofibrosis, or graft
                                                                                                                                                                                                                                                                                                                                                                                                                           paroxysoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal,
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RESULT 14 AAW47917 Percent Similarity:
Best Local Similarity:
Query Match: В Š B US-09-513-151-3 (1-2041) x AAW47911 (1-11) Alignment Scores: 1967 ACAGCAGTGATAATAACTCACACA 1944 stimulatory activity; immunosuppressant; Human; tumour necrosis factor; neutrophil; monocyte; macrophage; Human 09-JUN-1998 AAW47917 standard; peptide; 11 Synthetic AAW47917 Homo sapiens w ThrAlaValIleIleThrHisThr 10 tumour (first entry) necrosis factor derived peptide 1175. 150 8.00 100.00% 100.00% ₽ Mismatches: Conservative: Indels: Length: 000081

Key Modified-site

Location/Qualifiers /note= "nipocotic acid"

WO9748725-A1

20-JUN-1997; 24-DEC-1997.

97WO-AU00395

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Query Match:
                                                                                                                                                                                                                                                                           RESULT 15
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21-JUN-1996;
06-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mack
                                                                                                                                                                                                                                          AAW47901 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a peptide derived from a human to necrosis factor peptide. The peptide can have neutrophil and/or monocyte/macrophage stimulatory activity. The peptide is derived the sequence of tumour necrosis factor (TNF)-derived peptide 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 44; 65pp; English.
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WO9748725-A1
                                                                                                                                      Human tumour necrosis factor derived
                                                                                                                                                                         09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viral or protozoan infection, nocturnal, haemoglobinuria, 1
                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              administration of immunosuppressive drugs, and other bacterial,
                                                                                 stimulatory
                                                                                                    Human; tumour necrosis
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                                                                                                                                                                                                                                                                                                              ThrAlaValIleIleThrHisThr 10
                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               host disease.
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                                                                                 activity;
                                                                                                                                                                     (first entry)
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96AU-0000610.
96AU-0002165.
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8.00
100.00%
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                                                                                                                                                                                                                                          peptide; 11
                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                immunosuppressant;
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                                                                                                    factor; neutrophil;
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Matches:
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Indels:
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                                                                                                                                    peptide 1100
                                                                                   cancer;
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                                                                                                    monocyte;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             myelofibrosis,
                                                                                   /te; macrophage;
infection.
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Search completed: April Job time: 66.5 secs

21,

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                           Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a peptide derived from a human tumour concerns factor peptide. The peptide can have neutrophil and/or monocyte/macrophage stimulatory activity. The peptide is derived from the sequence of tumour necrosis factor (TNF) derived peptide 419 (PSTHVLITHTI; see AU74762/91 and 44664/93). It can have improved properties such as increased potency, extended in vivo half life or, continuity (class 1), equal neutrophil round monocyte/macrophage stimulatory activity (class 2), or preferentially enhanced monocyte/macrophage crimitatory activity (class 3). It can be used for the treatment or prevention of infections. In particular, it can be used for treating AIDS, cancer, diabetes, nosocomial infection, tuberculosis, cystic chirosis, community acquired pneumonia, meningitis, Mycobacteria, community acquired pneumonia, meningitis, Legionellosis, in particular, Pasteurellosis, Legionellosis, acquired for treating acqu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Histoplasmosis, Listeriosis, Pneumocystis carnii, Trypanosoma cruzi, coccidian parasitical infection, an inherited primary neutropenic disorder, an inherited primary defect of phagocytic cell function, an inherited secondary defect of phagocytic cell function, an acquired defect of phagocytic cell function, immunosuppression due to the administration of immunosuppressive drugs, and other bacterial, funging the control of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mack
1967 ACAGCAGTGATAATAACTCACACA 1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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21-JUN-1996;
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-CQ-/cgn2_1/USPT0_spool/US99513151/runat_15042003_141145_26426/app_guery.fasta_1.2446
-CQ-/cgn2_1/USPT0_spool/US99513151/runat_15042003_141145_26426/app_guery.fasta_1.2446
-CQ-/cgn2_1/USPT0_spool/US99513151_runat_1504200_1-MATRIX-blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE-LOCAL -OUTFMT=pto -NORN-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US99513151_eCGN1_pto -NORN-ext -15042003_141145_26426
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDXT=0.5 -FGAPOP=6
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## SUMMARIES

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NUMBER OF SEQ ID NOS: 2660 SOFTWARE: Patentin Ver. 2.0

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Sequence 2199, Application US/1022911
(GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PM001C1N
CURRENT APPLICATION NUMBER: US/10/222,911
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/757,028
PRIOR APPLICATION NUMBER: 09/757,028
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Query Match:
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; ORGANISM: Homo sapiens
US-09-757-028-2199
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                 Sequence 151, Application PC/TUS0207826
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
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LENGTH: 143
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PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
SOFTWARE: Patentin Ver. 2.0
FILE REFERENCE: MRI-030PC
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US-10-097-340-151
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; Sequence 151, Application US/10097340
; GENERAL INFORMATION:
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Best Local Similarity:
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
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SEQ ID NO 151
LENGTH: 465
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PRIOR FILING DATE: 2001-03-14
PRIOR PELICATION NUMBER: 60/32
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/31
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/32
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
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PRIOR FILING DATE: 2001-09-27
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Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
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Karen GLATT
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Robert C. BAST, Jr.
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                                                                           Score:
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LENGTH: 465
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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030PC
CURRENT APPLICATION NUMBER: PCT/US02/07826
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
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NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version
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PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/276,026
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FILING DATE: 2001/09/26
APPLICATION NUMBER: 60/311,732
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FILING DATE: 2001-09-26
APPLICATION NUMBER: 60/323,580
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APPLICATION NUMBER: 60/325,102
FILING DATE: 2001-09-26
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FILING DATE: 2001-08-10
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Percent Similarity:
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US-10-097-340-153
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 153
LENGTH: 467
TYPE: PRT
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
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PRIOR FILING DATE: 2001-09-26
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1 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGAGCGCACATAAAATCC
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Robert C. BAST, Jr
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Rachel E. MEYERS
Michael MORRISEY
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                                            Alignment Scores: Pred. No.:
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US-60-412-418-773
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Query Match:
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US-60-389-987-773
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LENGTH: 294
TYPE: PRT
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SEQ ID NO 773
LENGTH: 294
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APPLICANT: Fahy, E
APPLICANT: Zhang,
APPLICANT: Gibson,
APPLICANT: Taylor,
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CURRENT FILING DATE: 2002-09-20
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APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Daie E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TIPLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P3
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-06-17
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APPLICANT: Taylor, Steven W.
APPLICANT: Glen, Gary M.
APPLICANT: Glen, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465P2
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                                                                                                                                                 TYPE: PRT
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Zhang, Bing
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                     Alignment Scores: Pred. No.:
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Best Local Similarity:
Query Match:
                                                                             ORGANISM: Drosophila
US-60-173-464-8824
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US-60-173-464-8824
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US-60-167-217-10879
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Sequence 10879, Application US/60167217
GENERAL INFORMATION:
APPLICANT: Li, Peter W. D.
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Sequence 8824, Application US/601/3404
GENERAL INFORMATION:
GENERAL INFORMATION:
ILI, Petter W.D.
TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS
TITLE OF INVENTION: TRANSITY
                                                                                                                                                         CURRENT APPLICATION NUMBER: US/60/173,464
CURRENT FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 30269
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8824
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10879
LENGTH: 635
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CURRENT APPLICATION NUMBER: US/60/167,217
CURRENT FILING DATE: 1999-11-24
                                                                                                                         TYPE: PRT
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95 LysLysHisAlaAsnLysValLysArg 103
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US-10-264-049-3108
; Sequence 3108, Application US/10264049
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PCT-US01-18569-3108
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; LOCATION: (64)
; OTHER INFORMATION:
PCT-US01-18569-3108
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA133PCT
CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
                                                                                                                               GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA13:91
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
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                                CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
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NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 133
SEQ ID NO 133
TANDE: B45
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; Sequence 401, Application US/09976594
; GENERAL INFORMATION:
                                RESULT 14
US-09-976-594-401
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US-10-205-219-133
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APPLICANT: Pinnock, Robert TITLE OF INVENTION: Identification and Use of Molecules Implicated in FILE REFERENCE: WL-A-018200

Pain

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(1-90) x US-10-205-219-133 (1-845)

1 TGTGACCTCTGTGATCGAATCATTGGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60

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RESULT 15
US-10-153-668-450
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Query Match:
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; OTHER INFORMATION: Incyte ID No: 3676741CD1
US-09-976-594-401
                                      Pred. No.:
                                                  Alignment Scores:
                                                                                   ; ORGANISM: Homo sapiens
US-10-153-668-450
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 2001-157043
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR APPLICATION NUMBER: JP 2001-260681
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-30
                                                                                                                      SOFTWARE: PatentIn Ver.
SEQ ID NO 450
LENGTH: 847
TYPE: PRT
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APPLICANT: ISHIZAWA, Kenya
TITLE OF INVENTION: STAT6 Activating Gene
FILE REFERENCE: 1254-0207p
CURRENT APPLICATION NUMBER: US/10/153,668
CURRENT FILING DATE: 2002-05-24
CURRENT FILING DATE: 18 60/203 172
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APPLICANT: Burbhinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-313175
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOTWARE: Patentin Ver. 2.0
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2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-135-8780 Sequence 8780, 4 63 38.4 847 7 US-60-949-016-11423 Sequence 17423, 5 US-09-949-016-11423 Sequence 17423, 5 US-09-724-676-49882 Sequence 17423, 5 US-09-724-676-4982 Sequence 49882, 7 34.8 597 5 US-09-724-676-4982 Sequence 49882, 5 US-09-724-676-49880 Sequence 49882, 5 US-09-724-676-49875 Sequence 49880, 5 US-09-724-676-49875 Sequence 49875, 5 US-09-724-676-49878 Sequence 49875, 5 US-09-724-676-49878 Sequence 49875, 5 US-09-724-676-49878 Sequence 49875, 5 US-09-724-676-49878 Sequence 49876, 5 US-09-724-676-49871 Sequence 49876, 5 US-09-724-676-49871 Sequence 49877, 5 US-09-724-676-49873 Sequence 49877, 5 US-09-724-676-49873 Sequence 49873, 5 US-09-724-676-49873 Sequen	72,	498	ñ	97 5 US-09-724-67.6A-4987	4.8 6	57	33
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2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 847 7 US-60-453-050-8780 Sequence 11423, 5 US-09-949-016-11423 Sequence 11423, 5 US-09-675-784A-9300 Sequence 11423, 5 US-09-724-676-49882 Sequence 49882, 7 34.8 597 5 US-09-724-676-49882 Sequence 49882, 5 US-09-724-676-49880 Sequence 49880, 5 US-09-724-676-49875 Sequence 49880, 5 US-09-724-676-49875 Sequence 49878, 5 US-09-724-676-49875 Sequence 49878, 5 US-09-724-676-49875 Sequence 49878, 5 US-09-724-676-49876 Sequence 49878, 5 US-09-724-6764-49876 Sequence 49878, 5 US-09-724-6764-49876 Sequence 49878, 5 US-09-724-6764-49876 Sequence 49878, 5 US-09-724-6764-49876 Sequence 49881, 5 US-09-724-6764-49877 Sequence 49877, 5 US-09-724-6764-49877 Sequence	73,	498	Sequence	96 5 US-09-724-676-4987	4.8 6	57	30
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3 8.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 242 5 US-09-724-676-4982 Sequence 49882, 7 57 34.8 597 5 US-09-724-676-49880 Sequence 49882, 7 57 34.8 646 5 US-09-724-676-49880 Sequence 49882, 8 57 34.8 646 5 US-09-724-676-49890 Sequence 49880, 9 57 34.8 647 5 US-09-724-676-49875 Sequence 49887, 1 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 3 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 3 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 4 57 34.8 649 5 US-09-724-676-49876 Sequence 49878, 5 57 34.8 649 5 US-09-724-676-49876 Sequence 49878, 5 57 34.8 649 5 US-09-724-676-49876 Sequence 49876, 5 57 34.8 649 5 US-09-724-676-49876 Sequence 49878, 5 57 34.8 652 5 US-09-724-676-49881 Sequence 49878, 5 57 34.8 652 5 US-09-724-676-49881 Sequence 49881, 7 57 34.8 652 5 US-09-724-676-49881 Sequence 49881, 7 57 34.8 652 5 US-09-724-676-49881 Sequence 49881,	77,	498	Sequence	59 5 US-09-724-676-49877	4.8 6	57	28
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2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 US-09-675-784A-9300 Sequence 11423, 5 US-09-754-676-49882 Sequence 9300, 5 US-09-724-676-4982 Sequence 49882, 7 34.8 597 5 US-09-724-676-4982 Sequence 49882, 5 34.8 646 5 US-09-724-676-49880 Sequence 49880, 646 5 US-09-724-676-49875 Sequence 49875, 34.8 647 5 US-09-724-676-49878 Sequence 49878, 5 34.8 647 5 US-09-724-676-49878 Sequence 49878, 5 34.8 647 5 US-09-724-676-49878 Sequence 49878, 5 34.8 649 5 US-09-724-676-49876 Sequence 49876, 5 US-09-724-676-49876 Sequence 49876, 5 US-09-724-676-49876 Sequence 49876, 5 US-09-724-6768-49876 Sequence 49876, 5 US-09-724-6	18	498	Sequence	52 5 US-09-724-676-4988	4.8 6	57	26
3 8.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 597 5 US-09-724-676-4982 Sequence 49882, 7 57 34.8 597 5 US-09-724-676-4980 Sequence 49882, 8 597 34.8 597 5 US-09-724-676-4980 Sequence 49882, 9 57 34.8 646 5 US-09-724-676-4980 Sequence 49880, 9 57 34.8 646 5 US-09-724-676-4987 Sequence 49879, 1 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 3 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 3 57 34.8 647 5 US-09-724-676-49878 Sequence 49878, 5 57 34.8 647 5 US-09-724-6768-49878 Sequence 49878, 5 57 34.8 649 5 US-09-724-6768-49878 Sequence 49878, 5 57 34.8 649 5 US-09-724-6768-49878 Sequence 49878,	76,	498	Sequence	49 5 US-09-724-676A-4987	4.8 6	57	25
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-943-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 5 7 34.8 597 5 US-09-724-676A-49882 Sequence 49882, 5 7 34.8 597 5 US-09-724-676A-49882 Sequence 49880, 5 7 34.8 646 5 US-09-724-676A-49880 Sequence 49880, 5 7 34.8 647 5 US-09-724-676A-49875 Sequence 49875, 5 7 34.8 647 5 US-09-724-676A-49875 Sequence 49875, 5 34.8 647 5 US-09-724-676A-49875 Sequence 49875, 5 34.8 647 5 US-09-724-676A-49878 Sequence 49878, 5 13 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	76,	498	Sequence	49 5 US-09-724-676-4987	4.8 6	57	24
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3 8.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 597 5 US-09-724-676-4982 Sequence 4982, 7 57 34.8 597 5 US-09-724-676-4980 Sequence 49882, 8 57 34.8 597 5 US-09-724-676-4980 Sequence 49880, 9 57 34.8 646 5 US-09-724-676-4980 Sequence 49880, 10 57 34.8 647 5 US-09-724-676-49875 Sequence 49875, 11 57 34.8 647 5 US-09-724-676-49878 Sequence 49878,	75,	498	Sequence	47 5 US-09-724-676A-4987	4.8 6	57	22
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-135-8780 Sequence 8780, 4 63 38.4 847 7 US-60-453-010-8780 Sequence 1780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 5 5 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 597 5 US-09-724-676-49882 Sequence 49882, 7 34.8 597 5 US-09-724-676A-49882 Sequence 49882, 8 57 34.8 546 5 US-09-724-676A-49880 Sequence 49880, 9 57 34.8 646 5 US-09-724-676A-49875 Sequence 49880, 57 34.8 647 5 US-09-724-676A-9880 Sequence 498875, 8 57 34.8 647 5 US-09-724-676A-9880 Sequence 49880, 57 34.8 647 5 US-09-724-676A-9880 Sequence 498875, 8 57 34.8 647 5 US-09-724-676A-98875	78	498	Sequence	47 5 US-09-724-676-4987	4.8 6	57	21
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 38.4 847 7 US-60-453-0135-8780 Sequence 8780, 4 63 38.4 847 7 US-60-453-0135-8780 Sequence 18780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 US-09-675-784A-9300 Sequence 9300, 5 14.8 597 5 US-09-724-676-49882 Sequence 49882, 5 14.8 597 5 US-09-724-676-49882 Sequence 49880, 5 14.8 597 5 US-09-724-6764-49880 Sequence 49880, 5 14.8 597 5 US-09-724-676A-49880 Sequence 49880, 5 14.8 597	75,	498	equenc	47 5 US-09-724-676-4987	4.8 6	57	20
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2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 597 5 US-09-724-676-49882 Sequence 49882, 7 57 34.8 597 5 US-09-724-676A-49882 Sequence 49882, 7	98	498	Sequence	46 5 US-09-724-676-4988	4.8 . 6	57	18
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300, 6 57 34.8 597 5 US-09-724-676-49882 Sequence 49882,	82,	498	Sequence	97 5 US-09-724-676A-4988	4.8 5	57	17
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-058-780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423, 5 57 34.8 242 5 US-09-675-784A-9300 Sequence 9300,	82,	498	Sequence	97 5 US-09-724-676-4988	4.8 5	. 57	16
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780, 4 63 38.4 853 5 US-09-949-016-11423 Sequence 11423,	,0	930	equenc	42 5 US-09-675-784A-930	4.8 2	57	15
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780, 3 63 38.4 847 7 US-60-453-050-8780 Sequence 8780,	23,	114	Sequence	53 5 US-09-949-016-1142	8.4 8	63	14
2 63 38.4 847 7 US-60-453-135-8780 Sequence 8780,	ç	878	Sequence	47 7 US-60-453-050-878	8.4 8	63	13
	٥	878	Sequence	47 7 US-60-453-135-878	8.4 8	63	12

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US-09-513-151-3_COPY_1121_1210 (1-90) x US-60-453-135-7969 (1-85)
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7969
LENGTH: 85
TYPE: PRT
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APPLICANT: VIAKOUBOVA, O19a
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREO
61 AAATCCCACTTGAACCAACTGAAGAAAAGA 90
                                                                                                     1 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
                                                                        CysAspLeuCysAspArgIleIleIleGlyAspArgGluTrpAlaAlaHisIleLysSer
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Matches:
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Best Local Similarity: Query Match:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-7967
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7967
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001456
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7969
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TYPE: PRT
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Sequence 563, Application US/10380731
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-114
CURRENT APPLICATION NUMBER: US/10/380,731
CURRENT FILING DATE: 2003-03-14
CURRENT FILING DATE: 2003-03-16
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-731-563
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                                                                               US-09-513-151-3_COPY_1121_1210 (1-90) x US-10-380-731-563 (1-411)
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-050-7967
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                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/659,671
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 888
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
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                               1 TGTGACCTCTGTGATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
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                                                                  US-09-513-151-3_COPY_1121_1210 (1-90) x US-60-453-050-7968 (1-475)
                                                                                                                     Query Match:
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Best Local Similarity:
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7968
LENGTH: 475
TYPE: PRT
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APPLICANT: IAKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILLING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7968
LENGTH: 475
TYPE: PRT
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APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: STEMOSIS, METHODS OF
FILE REFERENCE: CL001457
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                                   TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
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PCT-US02-41115-54
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                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
PCT-USO2-41115-54
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: PCT/US02/41115
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US 60/343,004
PRIOR ETLING DATE: 2001-12-19
PRIOR ETLING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/347,633
PRIOR FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: US 60/351,749
PRIOR ETLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/359,498
PRIOR ETLING DATE: 2002-02-22
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                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 114
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TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1338 PCT
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TYPE: PRT
ORGANISM: Homo sapiens
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75 CysLysValCysCysAlaLeuLeuIleSerGluSerGlnLysLeuAlaHisTyrGlnSer
                           1 TGTGACCTCTGTGATCGATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
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BURFORD, Neil
ELLIOTT, Vicki S.
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KHARE, Reena
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61 AAATCCCACTTGAACCAACTGAAGAAA 87

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Alignment Scores: Pred. No.:
                                                           ; NAME/KEY: VARIANT
; LOCATION: (1)...(294)
; OTHER INFORMATION: Xaa -
US-60-452-680-16040
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Best Local Similarity:
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US-10-218-140-3448
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US-10-218-140-3448
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APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16040
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 16040, Application US/60452680 GENERAL INFORMATION:
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PRIOR FILING DATE: 1999-04-05
PRIOR APPLICATION NUMBER: 60/127,636
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: 60/127,607
PRIOR FILING DATE: 1999-03-31
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                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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LysLysHisAlaAsnLysValLysArg 103
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                                                                              Any Amino Acid
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Query Match:
                                                                                                 US-09-513-151-3_COPY_1121_1210 (1-90) x PCT-US03-07002-35 (1-339)
                                                                                                                                                                                                                                            Pred. No.:
                                                                                                                                                                                                                                                           Alignment Scores:
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; OTHER INFORMATION: Incyte ID No.: 7509991CD1
PCT-US03-07002-35
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SEQ ID NO 35
LENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KHARE, Reena; LEE, Sally;
APPLICANT: BECHA, Shanya D.; LEE, Soo Yeun
TITLE OF INVENTION: NUCLEIC ACID-ASSOCIATED PROTEINS
FILE REFERENCE: PF-1377 PCT
CURRENT APPLICATION NUMBER: PCT/US03/07002
CURRENT FILING DATE: 2003-03-05
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PRIOR APPLICATION NUMBER: US 60/362,329
PRIOR FILING DATE: 2002-03-06
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                   293 CysSerIleCysAspLeuProValHisSerAsnLysGluTrpSerGlnHisIleAsnGly 312
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LEE, Ernestine A.; KHAN, Farrah A.;
YUE, Henry; FORSTHE, Ian J.;
RAMKUWAR, Jayalaxmi; GRIFFIN, Jennifer A.;
LI, Joana X.; MARQUIS, Joseph P.;
LEHR-MASON, Patricia M.; JIN, Pei;
HAWKINS, Phillips R.; WILSON, Amy D.;
SWARNAKAR, Anita; HE, Ann;
BWARNAKAR, Anita; HE, Ann;
DUGGAN, Brendan M.; EMERLING, Brooke M.;
DUGGAN, Brendan M.; EMERLING, Brooke M.;
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Best Local Similarity:
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US-60-453-135-8780
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US-60-453-050-8780
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CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 8780
LENGTH: 847
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8780, Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
TITLE OF INVENTION: STENOSIS, METHODS OF
FILE REFERENCE: CL001457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -60-453-135-8780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CARGILL, Michele APPLICANT: IAKOUBOVA, Olga
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                       LENGTH: 847
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293 CysSerIleCysAspLeuProValHisSerAsnLysGluTrpSerGlnHisIleAsnGly 312
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                                          1 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
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US-09-949-016-11423
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Alignment Scores
                                   ; ORGANISM: Aspergillus fumigatus US-09-675-784A-9300
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US-09-949-016-11423
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                  NUMBER OF SEQ ID NOS: 13925
SEQ ID NO 9300
LENGTH: 242
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                                                                                                                                                                  CURRENT FILING DATE: 2000-09-29 PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29
                                                                                                                                                                                                                                      APPLICANT: GREENE, JONATHAN R.

TITLE OF INVENTION: ASPERGILLUS FUMIGATUS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020US1
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/675,784A
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CURRENT FILING DATE: 2000-04-14
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TYPE: PRT
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NOLLING, JORK
ZENG, QIANDONG
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Search completed: April 21, 2003, 18:58:58 Job time : 4.07555 secs	Qy 61 AAATCCCACTTGAACCAACTGAAG 84 ::::::    Db 227 ArgAlaHisLysArgAlaIleLys 234	Qy 1 TGTGACCTCTGT	US-09-513-151-3_COPY_1121_1210 (1-90) x US-09-675-784A-9300 (1-242)	Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Ouery Match: DB:
.1 21, 2003, 18 %	AAATCCCACTTGAACCAACTGAAG 84 :::::    :::    argalaHisLysargalaIleLys 23	TGTGACCTCTGTGATCGAATCAT    :::::     ysGluIleCysSerArgThrMetAl	121_1210 (1-90	10.3 57.00 53.57% 25.00% 34.76%
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-LOOPEXT-0 -LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09513151_@CGN_1_1_15_@runat_15042003_141145_26460
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG-
-DEV_TIMEGUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDP-10 -XGAPDEXT-0.5 -FGAPOP-6
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                      Sequence 731,
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                                                                                                                     Description
Sequence 901,
                                             Alignment Scores: Pred. No.:
                                                                                                                     ; ORGANISM: HOMO US-10-102-806-731
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Sequence 5, Appli Sequence 44, Appl	equence 16,	equence 15, App	equence 18	130 Appr	) N	equence 28, Appl	6	11466,	N	Sequence 2, Appl	30, Appl	_ 0	e Z, Appi	883, App	10	Ņ	2 70	66	12	10	4	1192, Ap	ω	Sequence 43910,	29, Appl	Sequence 2, Appli	equence 2, Appli	2	equence 11	equence 2, Appli	92, 7	Sequence 679, Ap	571 App	e 1441	equence 1012 A	ermence 300 An

## ALIGNMENTS

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US00/05881 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
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                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 846
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  3.53
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Length:
Matches:
Conservative:
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 143 Human Secreted Proteins
FILE REFERENCE: PS500P1
CURRENT APPLICATION NUMBER: US/09/986,480
CURRENT FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: PCT/US00/12788
PRIOR APPLICATION NUMBER: US 60/134,068
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
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SEQ ID NO 246
LENGTH: 123
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                                                                                                                                                                                                                 Sequence 368, Application US/09986480 Publication No. US20030027999A1
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NUMBER OF SEQ ID NOS:
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US-09-764-864-901
; Sequence 901, Application US/09764864
; Patent No. US20020132753A1
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Pred. No.:
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NUMBER OF SEO ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 901
LENGTH: 238
TYPE: PRT
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CURRENT FILING DATE: 2001-01-17
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                                                                                                                                                          Sequence 1012, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
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APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
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                                                                                                   APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and FILE REFERENCE: PTZ23
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Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792 SOFTWARE: PatentIn Ver. 2.0
                                                        CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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US-09-764-864-1441
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; LENGTH: 206
; TYPE: PRT
; ORGANISM: Homo :
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US-09-764-864-1441
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1141
LENGTH: 206
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                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
  CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
                                                                                APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
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US-09-513-151-3_COPY_1121_1210 (1-90) x US-09-925-302-679
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Best Local Similarity:
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Patent No. US20020049941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
SEQ ID NO 679
LENGTH: 179
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                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 896
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                             LENGTH: 17
TYPE: PRT
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NAME/KEY: SITE
LOCATION: (179)
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OTHER INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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PRIOR APPLICATION NUMBER: US 60/249,305
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/251,364
PRIOR FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: US 60/289,172
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2001-05-07
PRIOR FILING DATE: 2001-05-07
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US-09-866-562-92
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LENGTH: 229
TYPE: PRT
                   SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09999248 Patent No. US20020176852A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                APPLICANT: Lambeth, J. David
APPLICANT: Cheng, Guangjie
TITLE OF INVENTION: Mitogenic Oxygenase Regulators
FILE REFERENCE: 05501-0180 43150-266489
CURRENT APPLICATION NUMBER: US/09/999,248
CURRENT FILING DATE: 2001-11-15
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                                                               NUMBER OF SEQ ID NOS:
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CURRENT FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 96
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APPLICANT: Klee, Jennifer
APPLICANT: Switzer, Anne
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
FILE REFERENCE: 210121.502
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ENGTH: 578
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Klee, Jennifer
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ORGANISM: Homo sapiens

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Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-101-464A-114
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                                                                                                Sequence 2, Application US/10105695 Publication No. US20020197272A1 GENERAL INFORMATION:
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SEQ ID NO 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/101.464A CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 09/704.302 PRIOR FILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR FILING DATE: 1999-01-12 PRIOR APPLICATION NUMBER: 60/162,866 PRIOR FILING DATE: 1999-11-01 PRIOR FILING DATE: 1999-11-01 PRIOR FILING DATE: 1999-11-01
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of FILE REFERENCE: 11000.1020c2
                  APPLICANT: Galloway, Darrel R.
APPLICANT: Mateczun, Alfred J.
TITLE OF INVENTION: Methods for Protection
FILE REFERENCE: 22727/04115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US00/00724 PRIOR FILING DATE: 2000-01-11
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FILE REFERENCE: 22727/04115
CURRENT APPLICATION NUMBER: US/10/105,695
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    Sequence 2, Application US/09747521 Patent No. US20020051791A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: BO2
TYPE: PRT
ORGANISM: Bacillus anthracis
US-10-105-694-2
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US-10-105-694-2
RESULT 15
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LENGTH: 809
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PRIOR APPLICATION NUMBER: US 09/747,521
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/105,694
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: US 09/747,521
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Galloway, Darrel R.
APPLICANT: Mateczun, Alfred J.
TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacill FILE REFERENCE: 22727/04116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
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                                                      333 IleGluProLysLysAsp 338
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APPLICANT: Galloway, Darrel
APPLICANT: Mateczun, Alfred
ITILE OR INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
FILE REPERENCE: 22727/04079
CURRENT PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 8
SOSTWARRE: Patentin version 3.0
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-Q-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141144_26406/app_query.fasta_1.2446
-Q-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141144_26406/app_query.fasta_1.2446
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-LOOPEXT=0 -UNITS_bits -START=1 -END-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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US-09-288-143-190

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Patent No. 6054295
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
FILE REFERENCE: 19999Y
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                                                        244 CysAspLeuAlaAspArgGluLeuValValIleIleGly-----TrpAlaLysHis
261 IleProGlyPheSerSerLeuSer 268
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US-08-970-120-025-2
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US-08-867-611-36
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Best Local Similarity:
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US-09-141-000-6
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PATENT NO. 6054295
GENERAL INFORMATION:
APPLICANT: Chen, Fang
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atent No. 5958710 GENERAL INFORMATION:
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                     SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acid
TYPE: amino acid
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
TOPOLOGY:
                                                                                           APPLICATION NUMBER: GB 9609576.5 FILING DATE: 08-MAY-1996
                                                                                                                                                     FILING DATE:
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5958710
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US-09-040-508-2
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                                                          Alignment Scores:
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 Percent Similarity:
Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                     NAME: PRESTIA, PAUL F
REGISTION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                             FILING DATE: 16-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION UNBER: US/09/040,508 FILING DATE: 17-MAR-1998
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                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: GB 9705451.4 FILING DATE: 17-MAR-1997 APPLICATION NUMBER: GB 9803289.9 FILING DATE: 16-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
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                                                                                                                                                   TYPE:
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                           Length:
Matches:
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Best Local Similarity:
Query Match:
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US-09-500-654-2
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CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: 9705451.4
EARLIER FILING DATE: 1997-03-17
EARLIER APPLICATION NUMBER: 9803289.9
EARLIER FILING DATE: 1998-02-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-141-000-4
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                                       ; ORGANISM: Human
US-09-141-000-4
Alignment Scores:
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Patent No. 6359116
GENERAL INFORMATION:
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APPLICANT: Chen, Fang
TITLE OF INVENTION: BECEPTOR PROTEINS
TITLE OF INVENTION: RECEPTOR PROTEINS
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                                                                                          SEQ ID NO 4
LENGTH: 458
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                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/141,000 CURRENT FILING DATE: 1998-08-26 NUMBER OF SEQ ID NOS: 30
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                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-443-184-50
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
US-09-443-184-50
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SOUTWARE: PERL Program
SEQ ID NO 50
LENGTH: 653
TYPE: PRT
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US-09-288-143-190
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Query Match:
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   GENERAL INFORMATION:
APPLICANT: Brewer et al.
TITLE OF INVENTION: 53 Human Secreted ProfeILE REFERENCE: PZ018P1
CURRENT APPLICATION NUMBER: US/09/288,143
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                                                                                              Sequence 190, Application US/09288143 Patent No. 6433139
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APPLICANT: Lal, Preeti
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                                                                                                                           Sequence 23, Application US/08679493A Patent No. 6303295
GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, OF THE REFERENCE: 55-95
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EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/071,498
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,527
EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,536
EARLIER FILING DATE: 1997-10-09
EARLIER FILING DATE: 1997-10-09
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 190
LENGTH: 136
                                                             CURRENT APPLICATION NUMBER: US/08/679,493A CURRENT FILING DATE: 1996-07-12 PRIOR APPLICATION NUMBER: 60/001203 PRIOR FILING DATE: 1995-07-14
             PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EARLIER APPLICATION NUMBER: 60/061,532 EARLIER FILING DATE: 1997-10-09
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OTHER INFORMATION:
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LOCATION: (42)
OTHER INFORMATION: Xaa
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LOCATION: (121)
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PatentIn Ver.
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                                                                                                                                           SELENOPROTEINS, CODING SEQUENCES AND METHODS
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US-08-021-601-2
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Best Local Similarity:
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Best Local Similarity:
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; LOCATION: (1)..(226)
; OTHER INFORMATION: X
US-08-679-493A-23
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                                                                                                                                                    Sequence 2, Application US/08021601 Patent No. 5591631
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GENERAL INFORMATION:
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LENGTH: 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant C
TITLE OF INVENTION: And Their Use in the Modification
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
                                                                                                                                        GENERAL INFORMATION:
                                                                                APPLICANT:
APPLICANT:
APPLICANT:
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                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                    APPLICANT:
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 ADDRESSEE:
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                                                   Arora, Naveen
Singh, Yogendra
VENTION: ANTHRAX
                                                                                             Klimpel, Kurt R.
Nichols, Peter J.
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Needle & Rosenberg, P.C
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                                        RELATED
                                        TOXIN FUSION PROTEINS METHODS
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Matches:
Conservative:
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n of Plant Cell Signalling
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COUNTRY:

Georgia Y: USA Atlanta

30303

STREET:

133 Carnegie Way, Suite 400

US/08/082,849B

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Percent Similarity:
Best Local Similarity:
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tent No. 5677274
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
NAME
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 94111-3834
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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                               ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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 FELECOMMUNICATION INFORMATION:
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                                                                                    APPLICATION NUMBER: FILING DATE: June CLASSIFICATION:
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ZIP: 94105
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STATE: CA
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REFERENCE/DOCKET NUMBER: 15
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Steuart Street Tower, 20th Floor, One Market
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Singh, Yogendra
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PCT-US94-01624-2

MOLECULE TYPE:

protein

ropology:

amino acid )GY: linear

TELEFAX: (415) 543-9600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 776 amino

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; LENGTH: 878
; TYPE: PRT
; ORGANISM: HOMO S
US-09-735-934A-2
                                                                                                                                                          RESULT 15
US-09-135-782-4
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Query Match:
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                   GENERAL INFORMATION:
APPLICANT: XU, Shuang-yong
TITLE OF INVENTION: Method For Cloning and Producing The NspI Restriction
TITLE OF INVENTION: Endonuclease In E. coli and Purification Of The
TITLE OF INVENTION: Recombinant NspI Restriction Endonuclease
FILE REFERENCE: NEB-143
                                                                                                                        Sequence 4, Application US/09135782 Patent No. 6027929
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TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO0851
CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
CURRENT APPLICATION NUMBER: US/09/135,782
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; ORGANISM: NO.
US-09-135-782-4
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SEQ ID NO 4
LENGTH: 244
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                                                                  95
                                                                                              61 AAATCCCACTTGAACCAACTG 81
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Result
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-Q=/Cgn2_1/USPTO_spoo1/US09513151/runat_15042003_141144_26380/app_query.fasta_1.2446
-Q=/Cgn2_1/USPTO_spoo1/US09513151/runat_15042003_141144_26380/app_query.fasta_1.2446
-DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=n2p.rspt -MINMATCH=0,1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALICN=15
-MODE=LOCAL -OUTEMT=pto -NORESTIZE=500 -MINLEN=0 -MAXLEN200000000
-USER=US09513151_@CGN_1_1_25_@runat_15042003_141144_26380 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPDATO - 5 -FGAPOP=6 -FGAPEXT=7
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Maximum DB
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Q96fj3 homo sapien
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010741; AAH10741.1;
InterPro; IPR002627; IPPT.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
SMART; SM00355; ZnF_C2H2; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
                                                                                                                                                                                                                     Q96FJ3 PRELIMINARY; PRT; 324 AA.
Q96FJ3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Similar to tRNA isopentenylpyrophosphate transferase.
                                                                                                                                 TISSUE-UTERUS;
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Transferase
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                       NCBI_TaxID=9606;
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Q8VTU9
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Q8VEH2
Q8ZCD7
Q9HIL4
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084925 plum pox vi
096nc0 homo saplen
09cpv7 mus musculu
08veh2 mus musculu
08veh2 mus musculu
08zcd7 yersinia pe
09hil4 thermoplasm
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Q8w374 oryza sativ
Q8s9z6 oryza sativ
Q94540 drosophila
Q9va29 drosophila
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Q9r0b7 mus musculu
Q42147 xencpus lae
Q9vhm6 drosophila
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Q9btg3 homo sapien
Q9h868 homo sapien
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Q9vz07 drosophila
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Q95u26 drosophila
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A Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shli
A Tanaka T., Nakamura Y., Isogano S.;
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AKO00068; BAA90923.1;
R InterPro; IPR002627; IPPT,
R InterPro; IPR000822; Znf_CZH2.
R Fofam; PF01715; IPPT; 1.
R Pfom; PF01715; IPPT; 1.
R ProDom; PD004674; IPPT; 1.
R PROSITE; PS00028; ZINC_FINGER_CZH2_1; UNKNOWN_1.
R PROSITE; PS00028; ZINC_FINGER_CZH2_1; UNKNOWN_1.
   Q96L45;
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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01-OCT-2000 (TYEMBLrel. 15, Last sequence update)
01-MAR-2002 (TYEMBLrel. 20, Last annotation update)
CDNA FLJ20061 fis, clone COL01383.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; l
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09H3H1;
01-MAR-2001
                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-20564178; PubMed-11111046;
Golovko A., Hjalm G., Sitbon F., Nica
"Cloning of a human tRNA isopentenyl
Gene 258:85-93(2000).

EMBL; AF074918; AAG331324.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barnes T., Hekimi S.;
"Regulation of Physiological Rates in Caenorhabditis elegans tRNA-Modifying Enzyme in the Mitochondria.";
Genetics 159:147-157(2001).
EMBL; AY052768; AALI4107.1;
InterPro; IPR002627; IPPT.
InterPro; IPR000822; Znf_C2H2.
Pfam; PF01715; IPPT; 1.
                                                                                     Pfam; PF01715; IPT; 1.
Probom; PD004674; IPPT; 1.
TIGREPAMS; TIGR00174; mlaA; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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ProDom; PD004674; IPPT; 1.
SMART; SM00355; ZnF_C2H2; 1.
TIGRFAMS; TIGR00174; miaA; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1;
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InterPro; IPR000822; Znf_C2H2.
Pfam; PF01711; IPPT; 1
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                        Transferase
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Primates;
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                                                     52725
                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
   .42e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B., Webb A.,
                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                       634469919D7F56A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2279AE7C2D999FF1 CRC64;
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Matches:
Conservative:
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Indels:
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    Percent Similarity:
Best Local Similarity:
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KARWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Shiburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Shiburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Havashtar P., Toyohida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                              ProDom; PD004674; IPPT; 1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

SEQUENCE 326 AA; 37191 MW; 454367A8B70DD1F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK003556; BAB22853.1; -
EMBL; BC019812; AAH19812.1; -
EMBL; BC019812; AAH19812.1; -
EMBL; BC019812; EMBL; BC0198121; -
EMBL; BC019812; EMBL; EMBL; BC019812; EMBL; BC019812; EMBL; BC019812; EMBL; BC019812; EMBL; BC019812; EMBL; EMBL; EMBL/GENBAR, EMBL; EMBL/GENBAR, 
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STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-112178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001
01-MAR-2002
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                                                                                                                                     No.:
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"Functional annotation of a
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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17, Last sequence update)
20, Last annotation update)
RIKEN CDNA 2310075G14 gene).
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Sciurognathi; Muridae;
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Matches: .
Conservative:
Mismatches:
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; Murinae; Mus
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DT 01
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                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY 2001) to the EMBL/GenBank/DDBJ datal
Submitted (MAY 2001) to the EMBL/GenBank/DDBJ datal
EMBL; BC007775; AAB07775.1; -
EMBL; BC007775; AAB07775.1; -
InterPro; IPR000802; Znf_C2H2.
InterPro; IPR003604; Znf_U1.
Pfam; PF00096; Zf-C2H2; 2.
Pfam; PF00096; Zf-C2H2; 4.
SMART; SM00355; ZnF_U1; 4.
SMART; SM00451; ZnF_U1; 4.
SMART; SM00451; ZnF_U1; 4.
SMART; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_4.
SMART; DNN-binding; Zinc-finger.
SEQUENCE 294 AA; 32932 MW; 095F02E19FBCFBEO CRO
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Q9UL40;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2002
Q9R0B7
Q9R0B7;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang M., May W.S., Ito T.; "JAZ requires the double-stranded RNA-binding zinc finger motifs nuclear localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded RNA-binding Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-99419013; PubMed-10488071;
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                                                                                                                                                     61 AAATCCCACTTGAACCAACTGAAGAAA
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
(TrEMBLrel. 13, (TrEMBLrel. 13,
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Last sequence update)
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            T DNA hybrids."; Linyer protein that specif J. Mol. Biol. 271:195-208(1997).

R EMBL; AF005083; AAC60260.1; -.
R InterPro; IPR000892; Znf_matrin.
R InterPro; IPR000690; Znf_matrin.
R InterPro; IPR003604; Znf_Ul.
R Ffam; PF00096; Zf-C2H2; 7.
SMART; SM00451; ZnF_U1; 7.
SMARR; SM00355; ZnF_C2H2; 7.
DNA-binding; Metal-binding; Zinc-finger.
SECHEMORE End. "."
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SMART; SM00451; ZnF_U1; 4.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_4.
DNA-binding; Zinc-finger.
DNA-binding; Zinc-finger.
SEQUENCE 294 AA; 32698 MW; 6BD916262EDBA71E
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
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01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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J. Biol. Chem. 274.27399-27406(1999).
EMBL; AF083339; AAD52017.1; -.
MGD; MGI:1349417; Zfp346.
InterPro; IPR000822; Znf_C2H2.
InterPro; IPR003604; Znf_U1.
Pfam; PF00096; Zf-C2H2; 3.
    SEQUENCE
                                                                                                                                                                                                                                                                                  MEDIJINE-97415754; PubMed-9268652; Finerty P.J. Jr., Bass B.L.; RA Xenopus zinc finger protein that
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MEDLINE-99419013; PubMed-10488071;
Yang M., May W.S., Ito T.;
"JAZ requires the double-stranded RNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Metal-binding; Z:
24 AA; 55588 MW;
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  104D86038ADB8D57 CRC64;
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RESULT
Q9VHM6
                   RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Addams N.D., Celniker S.E., Hichards S., Ashburner M., Handerson S.N., RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Handerson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Apbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Abril J.F., Apbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Ferriaz C., Ferriara S., Fleischmann W., RA Coldson K., Doup L.B., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Barris M., Durbin K.J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W., RA Gooson K., Doup L.B., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., Barris M., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Alasko P., Lei Y., Levitsky A.A., Li J., Hernandez J.R., Houck J., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Liin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liin X., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liin X., Lasko P., Lei Y., McGiner G., McLeod M.P., McPherson D.L., McLeod M.P., McPherson D.C., McLeod M.P., McP
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Ye J., Yeu...
Zheng X.H., Zhong J
Gibbs R.A., Myers
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAR-2002
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R EMBL; AE003680; AAF54277.1; -.

R HSSP; P1582; 1BBO.

R Flybase; FBgn0037618; CG11762.

R InterPro; IPR00082; Znf_C2H2.

R InterPro; IPR000892; Znf_Matrin.

R Pfam; PF00096; Zf-C2H2; 5.

R SMART; SM00355; ZNF_C2H2; 5.

R PROSITE; PS00058; ZNKC_FINGER_C2H2_1; 4.

R PROSITE; PS00058; ZNKC_FINGER_C2H2_2; 5.

R PROSITE; PS05057; ZNKC_FINGER_C2H2_2; 5.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.

SEQUENCE 314 AA; 36509 MW; C783E29DC50F5D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9GYG3; Q95UF6;
01-MAR-2001 (TIEMBLrel. 16, Created)
01-MAR-2002 (TIEMBLrel. 20, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
Hypothetical 49.5 kDa protein (TRNA isopentenyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9GYG3
                                                                                                                   Waterston R.;
"Direct Submission.";
Submitted (DEC-2001) to
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nemato Rhabditidae; Peloderinae;
Lemiaux J., Lakowski B., Webb A., Meng Y., Ubach A.,
Barnes T., Hekimi S.;
"Regulation of Physiological Rates in Caenorhabditis
tRNA-Modifying Enzyme in the Mitochondria.";
                                                        STRAIN-BRISTOL N2;
MEDLINE-21444833; PubMed-11560893;
                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                         "The sequence of C. elec
Submitted (NOV-1994) to
                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                               investigating biology. The C
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Connell M.;
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
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EMBL/GenBank/DDBJ databases.
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                                                                                                                                           Query Match:
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Q8W374;
Q1-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N., Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tsitrin T., Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbus Salzberg S.L., White O., Fraser C.M.; Salzberg S.L., White O., Fraser C.M.; "Oryza sativa chromosome 10 BAC OSJNBa0029C15 genomic sequence."; "Oryza sativa chromosome 10 BAC OSJNBa0029C15 genomic sequence."; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC087182; AAL59020.1; ".

InterPro; IPR003604; Znf_C2H2.

InterPro; IPR003604; Znf_C2H2.
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Interpro; IPR00822; Znf_C2H2.
Interpro; IPR00822; Znf_C2H2.
IPFT, IPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 29.2 kDa protein.
oSJNBA0029C15.17.
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EMBL; U13642; AAG00042.2; -.
EMBL; AY052773; AAL14112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzea; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
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::
                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 278 AA; 29241
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PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_2
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yta; Liliopsida; Poales; Po
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                                                           x Q8W374 (1-278)
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                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q94540;
Q94540;
           Cell 87:1271-1284(1996).

EMBL; U73125; AAB40721.1; -.

FlyBase; FBgn0017453; Zn72D.

InterPro; IPR000822; Znf_C2H2.
                                                                                                           Sauer F., Wassarman "TAF(II)s mediate ac embryo.";
                                                                                                                                                                                                                                                                                                                                                                    Zinc-finger protein ZN72D OR CG5215.
                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, 01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2002 (TrEMBLrel. 20, 21nc-finger protein ZN72D.
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Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similar to tRNA isopentenyltransferase.
OJ1656_A11.14.
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-97134673; PubMed-8980233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Oryza sativa nipponbare(GA3) genomic DNA, clone:OJ1656_A11.";
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NCBI_TaxID=39947;
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LysGlnHisLeuHisArgLeuArg
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IPR000690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
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Last annotation updat
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                                                                                                                              G.M., Tjian R.
transcription
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a; Poales; Poaceae;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar t W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Kalush F., Karpen G.H., Xe Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Matush F., Karpen G.H., Li J., Li Z., Liang Y., Lin X.,
RA Harris N.C., McDharos T.G., McDeod M.P., McDherson D.,
RA Mount S.M., Wolson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Ra Harris N.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Samer M. W., Schon R., Nixon K., Nusskern D.R., Pacleb J.M.,
Ra Charley M. S., San S., Pollard J., Puri V., 
RESULT 14
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Pred. No.:
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Q9VA29;
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Pterygota; Neoptera;
Ephydroidea; Drosophi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00355; ZnF_C2H2; 3.
SMART; SM00451; ZnF_U1; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_3
DNA-binding; Zinc-finger
SEQUENCE 558 AA; 61157 MW; 5DC76C1BEF2DC784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG12071 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel, 01-MAY-2000 (TrEMBLrel, 01-JUN-2002 (TrEMBLrel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
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Pfam; PF00096; Zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysGluLeuCysAspValThrCysThrGlyThrAspAlaTyrAlaAlaHisValArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10731132;
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58.00
53.57%
35.71%
35.37%
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ilidae; Drosophila.
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13,
21,
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Last annotation updat
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Gaps:
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Spier E., Sp. Svirskas R.,

Spradling A.C., Stapleton M., Strong R., Sun E., Tector C., Turner R., Venter E., Wang A.H., Wang

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Query Match:
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InterPro; IPR000822; Znf_C2H2.
Pfam; PF00096; zf-C2H2; 3
ProDom; PD000003; Znf_C2H2; 1.
SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 3.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 578 AA; 64636 MW; 19966A0D7BF;
                                                                                                                                       STRAIN-BERKELEY;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY058357, AAL13586.1;

FlyBase; FBgn0017453; Zn7ZD.

InterPro. IPR00082; ZnfCZD.

InterPro. IPR00082; ZnfCZH2.

Pfam; PF00096; Zf-C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001
01-DEC-2001
01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95U26
                                                                                                   DNA-binding; Zinc-finger. SEQUENCE 635 AA; 68457 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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ZN72D OR CG5215.
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62.50%
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Gaps:
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S., Zhu X., Smith H.O.,
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4
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Percent Similarity:
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Query Match:
Search completed: April 21, 2003, 18:55:43 Job time: 7.20225 secs
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                                                         275 AlaLysHisGlnLysValValLys
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                                                                                          61
                                                                                                                                                    1 TGTGACCTCTGTGATCGAATCATTGGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60
                                                                                          AAATCCCACTTGAACCAACTGAAG
                                                                                                                                                                                                               53.578
35.718
35.378
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unknown protein [i granzyme A (EC 3.4 granzyme A (EC 3.4

sarcosine oxidase

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ZK686.4 protein hypothetical translation elonga hypothetical prote

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steroid hormone probable carboxype DNA repair protein

probable iron upta cellulase (EC 3.2. cathepsin B mRNA 3

hypothetical prote hypothetical prote probable secreted ACMNPV orf122 - Bo probable iron

transcription regu probable dCTP deam hypothetical reverse transcript phenylalanine-tRNA hypothetical prote xylose operon tran

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Result
No.
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-Q-/Ggn2_1/USPTO_spool/US09513151/runat_15042003_141144_26390/app_query.fasta_1.2446
-DB=-PIR_73 -QFMT=-fastan -SUFFIX=-PIR_FIR_FIR_HANATCH=0.1 -LOOPEXT=0
-UNITS-bits -START=1 -END--1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST-45
-DCCALIGN=200 -THR_SCORE-PCt -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=-Pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09513151_@CGN_1_1_58_@runat_15042003_141144_26390 -NCPU-6 -ICPU-3
-NO_MAAP -LANGGUERY -NBG_SCORES-0 -WAI1 -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOD-10 -XGAPEXT-7
-YGAPPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXI-7
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Maximum DB
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-MODEL-frame+_n2p.model -DEV=xlh
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A;Gene: CESP:ZC395.6
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A; Residues: 1-433 <CON>
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                                               397 CysGluIleCysAsnIleSerMetThrGlyLysAspAsnTrpGlnLysHisIleAspGly 416
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## ALIGNMENTS

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R;Connell, M.
submitted to the EMBL Data Library, August 1994
A;Description: The sequence of C. elegans cosmid ZC395.
A;Reference number: Z20385
A;Accession: T27538
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A;Introns: 43/1; 201/1; 266/3; 310/2; 341/3; 377/3; 410/2
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                                                                                                                                                                                                                                                                                                                                                     EMBL:U13642; PIDN:AAB53886.1; GSPDB:GN00021; CESP:ZC395.6
be: strain Bristol N2; clone ZC395
                       Matches:
Conservative:
Mismatches:
Indels:
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seryl-tRNA synthetase (serS) homolog - Archaeoglobus fulgidus (;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec:1997 #sequence_revision 05-Dec:1997 #text_change 16-Jul-1999 C;Accession: B69504 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, R;Klenk, H.P.; Clayton, R;Klenk, H.P.; C
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C; Geneti
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-1A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69504
                                                                                                                                                           RINLEDK, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; D.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. Mature 390, 364-370, 1997
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A; Residues: 1·374,'R',376-428 <NAJ>
A; Residues: 1·374,'R',376-428 <NAJ>
A; Cross-references: EMBL:M15991
R; Cheret, G.; Bernardi, A.; Sor, F.
Yeast 12, 1059-1064, 1996
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A; Residues: 1-428 < CHW>
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A; Residues: 1-428 <CHE>
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R; Cheret, G.; Sor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: EMBL:X89633; NID:g1279694; PIDN:CAA61780.1; PID:g1419759:Note: the nucleotide sequence was submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Alternate names: protein O5447w;
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Xel69 (escapes X-inactivation) protein - hamster (fragment) C. Species: Cricetinae gen. sp. (hamster) C. Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_ch. C. Accession: I48129 # C. Accession: I48129 # C. Yen, P.H.; Mohandas, T.K.; Heng, H.I. Nature Genet. 7, 491-496, 1994 A. Title: The murine Xel69 gene escapes X-inactivation like A. Reference number: I48129; MUID:95038834; PMID:7951318
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148129
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C; Keywords: transmembrane protein
F;179-195/Domain: transmembrane #
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A;Gene: xe169
C;Superfamily: human retinoblastoma
                                                         zinc finger RNA binding protein, chromosome-associated - C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text.
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A;Tille: The murine Xel69 gene escapes X-inactivation like its human homologue.
A;Reference number: I48129; MUID:95038834; PMID:7951318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           escapes X-inactivation - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 26-May-2000
C;Accession: I84689
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A; Residues: 1-180 < RES>
                R; Meagher, M.J.; Schumacher, J.M.; Gene 228, 197-211, 1999
                                                                                                          T14343
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 A; Title:
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an ancient and highly conserved murine chromosome-assoc
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                               Edelhoff,
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A; Molecule type: mRNA
A; Residues: 1-1560 (*MUJ>
A; Cross-references: GB:L25270; NID:g457136; PID:g457137
A; Cross-references: GB:L25270; NID:g457136; PID:g457137
R; Agulnik, A.I.; Mitchell, M.J.; Mattei, M.G.; Borsani, G.;
Hum. Mol. Genet. 3, 879-884, 1994
Hum. Mol. Genet. 3, 879-884, 1994
A; Title: A novel X gene with a widely transcribed Y-linked
A; Reference number: I38235; MUID:95038739; PMID:7951230
A; Accession: I38235
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C;Date: 02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change 17-Mar-2000
C;Date: 02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change 17-Mar-2000
C;Accession: I54361; I38235
R;Wu, J.; Ellison, J.; Salido, E.; Yen, P.; Mohandas, T.; Shapiro, L.J.
Hum. Mol. Genet. 3, 153-160, 1994
A;Title: Isolation and characterization of XE169, a novel human gene that e.
A;Reference number: I54361; MUID:94214434; PMID:8162017
A;Accession: I54361
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A;Accession: T14343
A;Status: prellminary; translated from GB/EMBL/DDBJ
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Best Local Similarity:
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A; Residues: 1-1052 <MEA>
US-09-513-151-3_COPY_1121_1210
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A; Residues: 280-341,'Y', 343-344 < AGU>
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AGTTGGTTCAAGTGGGATTTGGATTTTATGTGCGCTGCCCATTCGCGATCCCCAATGATG

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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Rofe: see websites genome wusti.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: see websites genome wusti.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: G87721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein ZC123.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001
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                                                                                                                                              A;Gene: SPDB:SPCC550.15c
A;Map position: 3
C;Superfamily: zinc finger
                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                     zinc finger protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
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A; Residues: 1-263 <STO>
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A; Accession: T41390
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ce: strain 972h-;
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C:Keywords: phosphoprotein
F:10-122/Domain: response regulator homology <RRH>
F:61/Binding site: phosphate (Asp) (covalent) #status
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A; Residues: 1-481 <KAN>
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision
C;Accession: S74934
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N; Alternate names: protein slr0687
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   C; Genetics:
                    A; Cross-references:
                                    A; Molecule type: DNA
A; Residues: 1-379 < RAU>
                                                                          A;Status: preliminary
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A;Start codon: GTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko, T.; Sato, S.; Kotani,
K.; Okumura, S.; Shimpo, S.;
IA Res. 3, 109-136, 1996
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                    GB:L27649; NID:g497770; PIDN:AAA72427.1;
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C;Accession: C55205
R;Rauch, P.J.G.; de Vos, W.M.
J. Bacteriol. 176, 2165-2171, 1994
J. Hacteriol. 176, 2165-2171, 1994
A;Title: Identification and characterization of genes involved A;Reference number: A55205; MUID:94209213; PMID:8157585
A;Accession: C55205
                                                                                                                                                                                                                           integrase - Lactococcus lactis transposon Tn5276
C;Species: Lactococcus lactis
C;Date: 05-May-1995 #sequence_revision 05-May-1995 #text_change 15-Oct-1999
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Yamada, M.; Ya
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F;1804-1856/Product: protein 6K2 *status predicted F;1857-2292/Product: protein NIa *status predicted F;1857-2049/Product: Protein *status predicted F;1857-2049/Product: Protein *status predicted F;2293-2810/Product: protein NIb *status predicted F;2811-3140/Product: coat protein *status predicted F;1919/Binding site: phosphoryl-RNA (Tyr) (covalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: isolate PVV-SC
C;Superfamily: tobacco etch virus genome polyprotein
C;Keywords: ATP; coat protein; genome-linked protein; nucleotide binding; P-loop; phosph
F;1-308/Product: protein P1 #status predicted <P1P>
F;309-766/Product: protein HCpro #status predicted <HCP>
F;767-116/Product: protein P3 #status predicted <P3P>
F;1117-1168/Product: protein F3 #status predicted <CIP>
F;1117-1169-103/Product: protein GK1 #status predicted <CIP>
F;1169-103/Product: protein GK1 #status predicted <CIP>
F;1153-1260/Region: nucleotide-binding motif A (P-loop)
F;1338-1343/Region: nucleotide-binding motif B
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A;Residues: 1-3140 <MAI>
A;Cross-references: EMBL:X81083; NID:g531731; PIDN:CAA56974.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome polyprotein - plum pox virus (is N;Contains: coat protein; protein 6K1; C;Species: plum pox virus, PPV A;Variety: isolate PVV-SC C;Date: 20-Feb-1995 #sequence_revision
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Best Local Similarity:
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                                         CACTTGAACCAACTGAAGAAAAGA 90
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protein 6K1; protein 6K2;
, PPV
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  4 GACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAA
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Start codon: GTG
C;Superfamily: Methanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woest A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannas A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: H64422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: H64422
                                                                                                                                                                                                                              A; Gene: BH3032
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA repair protein BH3032 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-513-151-3_COPY_1121_1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type II restriction enzyme homolog - Methanococcus jannaschii
C; Species: Methanococcus jannaschii
                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AP001517; GB:BA000004;
A;Experimental source: strain C-125
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A;Residues: 1-222 <BUL>
US-09-513-151-3_COPY_1121_1210 (1-90)
                                                                                                                                                                                      Alignment Scores:
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A; Residues: 1-232 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U67541; GB:L77117; NID:g2826353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not
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Merrick, J.M.; Gloo
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63

GSPDB

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Db 208 GluLeuLeuAspHisValIleIleGlyAspArgThrPheValSer---LeuLysGluLys 226

Oy 64 TCCCACTTG 72

Db 227 GlyHisLeu 229
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Search completed: April 21, 2003, 18:51:12 Job time : 5.11168 secs

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-MODEL-frame+_n2p_model -DEV=x1h
-MODEL-frame+_n2p_model -DEV=x1h
-MODEL-frame+_n2p_model -DEV=x1h
-Q-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26366/app_query.fasta_1.2446
-Q-/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26366/app_query.fasta_1.2446
-DB=SwissProt_40 -QFMT-fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -STARR=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MIN=0 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -DOUBT-10 -NORM-ext -HEARSIZE=500 -MANLEN=2000000000
-USER-US09513151_@CGN_1_1_25_@runat_15042003_141143_26366 -NCPU=6 -TCPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Fgapop 6.0 , 1
Delop 6.0 , 1
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Compugen Ltd
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                                                                                                                                                                                                                          STRAIN-Sprague-Dawley;

MEDLINE=91236771; PubMed=2033075;

Belgrader P. Debed=2033075;

Belgrader P. Debed=2033075;

Molecular cloning of matrin 3. A 125-kilodalton protein of the nuclear matrix contains an extensive acidic domain.";

J. Biol. Chem. 266:9893-9899(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       xactus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
NCBI_TaxID=10116;
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01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                 EMBL; M63485; AAB63955
                                                                                                                                                                    -!- SUBCELLULAR LOCATION: NUCLEAR MATRIX.
-!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (RRM).
-!- SIMILARITY: CONTAINS 1 MATRIN-TYPE ZINC FINGER.
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YT32_CAEEL
NA95_HUMAN
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InterPro; IPR00
Pfam; PF00076;
                                         Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X., Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H., Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J., Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M., Huang G.-Y., Chen M.-D., Chen J.-L., "Gene expression profiling in the human hypothalamus-pituitary-adrenal axis and full-length cDNA cloning.";

Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
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ZN_FING
SEQUENCE
                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-Hypothalamus;
MEDLINE-20402571; PubMed-10931946;
                                                                                                                                                                                                             Nagase T., Ishikawa K.-I., Suyama M., Kikuno Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of uniden The complete sequences of 100 new cDNA clones for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                          MAT3_HUMAN STANDARD; PRT; 847 AA. P43243; Q9UQ27; Q9UHW0; O1-NOV-1995 (Rel. 32, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
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SMART; SM00355; ZnF_C2H2; 1.
SMART; SM00451; ZnF_U1; 2.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE; PS00030; RRM_RNP_1; FALSE_NEG PROSITE; PS50171; ZF_MATRIN; 1.

Nuclear protein; RNA-binding; Repeat;
            SEQUENCE OF 429-847 FROM N.A. MEDLINE-91236771; PubMed-2033075;
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                                                                                                                                                                                                                                                                                              TISSUE=Brain;
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Res. 5:277-286(1998).
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
MATRIN-TYPE.
, 5EA8D05529171238 CRC64;
                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Matches:
Conservative:
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CysSerIleCysAspLeuProValHisSerAsnLysGluTrpSerGlnHisIleAsnGly 312

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SMART; SM00360; RRM; 2.
SMART; SM00355; ZnF_C2H2; 1.
SMART; SM00451; ZnF_U1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular cloning of matrin 3. A 125-kilodalton protein nuclear matrix contains an extensive acidic domain."; J. Biol. Chem. 266:9893-9899(1991).
-i- EUNCTION: MAY PLAY A ROLE IN TRANSCRIPTION OR MAY INTOTHER NUCLEAR MATRIX PROTEINS TO FORM THE INTERNAL FI
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50102; RRM; 2.
PROSITE; PS501030; RRM_RRD_1; FALSE_NEG.
PROSITE; PS50171; ZE_MATRIN; 1.
Nuclear protein; RNA-binding; Repeat; 2
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InterPro; IPR003604; Znf_U1.
InterPro; IPR000690; Znf_matrin.
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EMBL; AF117236; AAF17217.1; -.
EMBL; M63483; -; NOT_ANNOTATED_CDS.
Genew; HGNC:6912; MATR3.
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-!- SIMILARITY: CONTAINS 2 RNA RECOGNITION MOTIFS (
-!- SIMILARITY: CONTAINS 1 MATRIN-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                 CONFLICT
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LIL -> IPV
Y -> C (IN
G -> P (IN
D -> H (IN
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P -> S (IN REF. 2).

P -> S (IN REF. 2).

EDFHGLLPKGYPHLCSICDLPVHSNKEWSOHINGASHSRRC OLLLEIYPEWNEDNDTGHTMGDPFMLQOSTNEAGILGPP PSFHLGGPAVEGRG -> YDYWHTLTERVIPTCALYVIGOP PSFHLGGPAVEGRG -> YDYWHTLTERVIPTCALYVIGOP TILIRSGYNISMEQVTVVDASFFLKSTQNGILTMIQDTQWVI
                                                                                                                                                                                                                                                                                                                                                                              RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
NUCLEAR LOCALIZATION
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MOD5_YEAST
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                            -i- FUNCTION: RESPONSIBLE FOR THE MODIFICATION OF A37 TO ISOPENTENYL A37 OF BOTH CYTOSOLIC AND MITOCHONDRIAL TRNAS.
-i- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate tRNA containing 6-isopentenyladenosine.
-i- PATHWAY: BIOSYNTHESIS OF THE MODIFIED BASE ISOPENTENYLADENOSINE
                                                                                                                                                                                                                                                                                                                                                                                                "Subcellular locations of MOD5 proteins: mapping of sequences sufficient for targeting to mitochondria and demonstration that mitochondrial and nuclear isoforms commingle in the cytosol."; Mol. Cell. Biol. 14:2298-2306(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gillman E.C., Slusher L.B., Martin N.C., Hopper A.K.; "MOD5 translation initiation sites determine N6-isopentenyladenosine modification of mitochondrial and cytoplasmic tRNA."; mol. Cell. Biol. 11:2382-2390(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92052176; PubMed=1946403;
Slusher L.B., Gillman E.C., Martin N.C., Hopper A.K.;
"mRNA leader length and initiation codon context determine
alternative AUG selection for the yeast gene MOD5.";
proc. Natl. Acad. Sci. U.S.A. 88:9789-9793(1991).
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"DNA sequence analysis of the VPH1-SNF2
Saccharomyces cerevisiae.";
Yeast 12:1059-1064(1996).
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P07834; Q12203;
P01-N05-1998 (Rel. 08, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
tRNA isopentenyltransferase (EC 2.5.1.8) (Isopentenyl-diphosphate:
tRNA isopentenyltransferase) (IPP transferase) (IPTase) (IPT).
                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: MITOCHONDRIAL, CYTOPLASMIC AND NUCLEAR.
-!- ALTERNATIVE PRODUCTS: TWO ISOFORMS MAY BE PRODUCED FROM THE U
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-87172703; PubMed-3031457;
EMBL; M15991;
                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE INITIATION, AND SUBCELLULAR LOCATION MEDLINE-91203856; PubMed=1850093;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hopper A.K.
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                                                                                   RC STÄAIN="VC-16 / DSM 4304 / ATCC 49558;

RX MEDLINE=98049343; PubMed=9389475;

RA Klenk H.-P., Clayton R.A., Fomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou J.

RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,

RA Cotton M.D., Spridgs T., Artiach P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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SGD;
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           venter J.C.;
"The complete genome sequence of the hyperthermophilic,
reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
-I- CATALYTIC ACTIVITY: ATP + L-serine + tRNA(Ser) - AMI
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ProDom; PD004674; IPPT; 1.
TIGRFAMs; TIGR00174; miaA; 1.
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EMBL; Z75182; CAA99499.1;
PIR; A26717; A26717.
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales
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Pfam; PF01715; IPPT; 1.
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15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Seryl-trnA synthetase (EC 6.1.1.11) (S
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FOR CYTOPLASMIC/NUCLEAR
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                                                                                                                                                                         Murakami Y., Naitou M., Hagiwara H., Shibata T., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda Yamazaki M., Tashiro H., Eki T.; "Analysis of the nucleotide sequence of chromoso Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFE4_YEAST
P43558;
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InterPro; IPR002317; tRNA-synt_ser.
Pfam; PF00587; tRNA-synt_2b; 1.
Pfam; PF02403; Seryl_tRNA_N; 1.
PRINTS; PR00981; TRNASYNTHSER.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 33.5 kDa protein in SEC53-FET5 1
                                                                                                 Nat. Genet. 10:261-268(1995).
-!- SIMILARITY: TO S.POMBE SPAC24C9.14.
-!- SIMILARITY: CONTAINS 1 OTU DOMAIN.
                                                                                                                                                                                                                                                                                                 STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
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                            between
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
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SMCX_CRIGR
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DT 01-FEB
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OG SMCX O
OS Cricet
OC CICET
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OC CACC
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RN 170
RP SEQUEN
RX MEDLIN
RA Wu J.,
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RA TOMONIO
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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95038834; F
Wu J., Salido E., Y
"The murine Xel69 g
homologue.";
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D50617; BAA09197.1; SGD; S0001850; YFL044C. InterPro; IPR003323; OTU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SmcX protein (Xe169 SMCX OR XE169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
DOMAIN 109
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SMART; SM00355; ZnF_C2H2;
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                                                              NON_TER
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                                                                                      L29564; AAA62383.1;
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Yen P., Mohandas T., Shapiro L.J.;
gene escapes X-inactivation like its
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; 32ABA3CFEA4BB5EB CRC64;
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     89D2A3C50B4A703A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIZ1_HUMAN STANDARD; PRT; 898 AA.
Q9ULV3; Q9Y3G0; Q9Y3F9; Q9UHK4; Q9YMM8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C1p1-interacting zinc finger protein (Nuclear CIZ1 OR NP94 OR LSFR1.
     InterPro; IPR00082; znf_C2H2.
InterPro; IPR003504; znf_U1.
InterPro; IPR003509; znf_matrin
SMART; SM00355; znf_C2H2; 2.
SMART; SM00451; znf_U1; 3.
                                                                            EMBL;
                                                                                                      EMBL;
EMBL;
                                                                                                                                                            modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                  between the Fugu and human genomes: implications for chrevolution and the cloning of disease genes.";

Hum. Mol. Genet. 8:1313-1320(1999).

-I- FUNCTION: MAY REGULATE THE SUBCELLULAR LOCALIZATION -
-I- SUBUNIT: INTERACTS WITH CIP/WAF1.

-I- SUBCELLULAR LOCATION: Nuclear.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND PRODUCED BY ALTERNATIVE SPLICING.
-I- SIMILARITY: CONTAINS 1 MATRIN-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 649-898 MEDLINE-99299247; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Medulloblastoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitsui K., Matsumoto A., Ohtsuka S., Ohtsubo M., Yoshimura A.; 
*Cloning and characterization of a novel p2l(Cipl/Wafl)-interacting
                                                                                                                                                                                                                                                                                                                                                                                                             Gilley J., Fried M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Warder D.E., Keherly M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20001941; PubMed-10529385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                              Extensive gene order differences within regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'NP94, a novel nuclear protein identified in a human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBI_TaxID=9606;
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                                                                         AF159025; AAF23231.1; ALT_INIT
AF2161; AAF37882.1; ALT_INIT
V17453; CAB44346.1;
V17454; CAB44347.1;
V17454; CAB44347.1;
                                                                                                                                  AB030835;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biophys. Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FEB-2000) to the
                                                                                                                                  BAA85783.1;
                                                                                                                                                                                                                                                                                                                                                                                                                         ## PubMed=10369878;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1),
MEDLINE-96438842; PubMed-8841177;
Kent-First M.G., Maffitt M., Muallem A.,
Ekenberg S., Agulnik A.I., Agulnik S.I.,
Abdul-Mawgood A., Vandeberg J.;
                                                                                                                                                                                                                                                                                                                                      Q9BY66; Q9HCU1; Q92509; Q92809;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
5mcY protein (Histocompatibility Y antigen) (H-Y).
SMCY OR HY OR HYA OR KIAA0234.
                      TISSUE=Bone marrow;
MEDLINE=97191544; PubMed=9039
Nagase T., Seki N., Ishikawa
                                                                                         Kent-First M.G., Maffitt M., Mualle
Ekenberg S., Agulnik A.I., Agulnik
Abdul-Mawgood A., Vandeberg J.;
Nat. Genet. 14:252-252(1996).
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                       SMCY_HUMAN
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                                                              SEQUENCE FROM N.A. (ISOFORM
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Nagase T., Seki N., ɪsɪɪɹɒɒɒ ... ...
Ohara O., Tanaka A., Kotani H., Miyajima
                                                                                                                                                                         Abdul-Mawgood A., Vandeberg J.; "Gene sequence and evolutionary Nat. Genet. 14:128-129(1996).
                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AAATCCCACTTGAACCAACTGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGTGACCTCTGTGATCGAATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysThrValCysAsnArgTyrPheLysThrProArgLysPheValGluHisValLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlnGlyH1sLysAspLysAlaLysGlu
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PS00028;
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ZINC_FINGER_C2H2_1; UNKNOWN_2.
                                      PubMed-9039502;
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34.76%
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Agulnik S.
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G -> S (IN REF.
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Matches:
Conservative:
Mismatches:
Indels:
                        Ohira M.,
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CRC64;

AAF23231). AAF23231). AAF37882).

AAF37882)

NP94B) NP94B)

Nomura

Kawarabayasi Y.,

of

SMCY.";

о. С., human

Shultz J. Bavister

B.,

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Shultz J. Bavister

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Pfam; PF00628; PHD; 4.
Pfam; PF02373; JmJC; 2.
Pfam; PF02375; JmJN; 1.
Pfam; PF02375; JmJN; 1.
SMART; SM00501; BRIGHT; 1.
SMART; SM00545; JmJN; 1.
SMART; SM00249; PHD; 2.
PROSITE; PS01159; ZF_PHD_1; 2.
PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poloumienko A., Blecher S.;

"Exon-intron structure of SMCX and SMCY genes in bovine and swine submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: May play a role in spermatogenesis (By similarity).

-i- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown here) and are produced by alternative splitcing.

-i- SIMILARITY: CONTAINS 1 ARID DOMAIN.

-i- SIMILARITY: CONTAINS 1 JMJC DOMAIN.

-i- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS:
  DOMAIN
ZN_FING
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long a modified and this statement is not removed entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97224581; PubMed-9060413; Agulnik S.I., Solovyev V.V.; Agulnik A.I., Bishop C.E., Lerner J.L., Agulnik S.I., Solovyev V.V.; "Analysis of mutation rates in the SMCY/SMCX genes shows that mammalian evolution is male driven."; Mamm. Genome 8:134-138(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sung R., Lin A.A., Hyman R.W., Vollrath L Cavalli-Sforza L., Oefner P.J.; "Population generic 1---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Population genetic implications from sequence variation chromosome genes."
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                                                                                                           DOMAIN
                                                                                                                     Zinc-finger;
                                                                                                                                                                                                                                                                                                                        MIM; 426000;
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                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                            AF273841; AAG00951.1; -. U52365; AAC51135.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ion of the coding sequences of unidentified human genes.
ing sequences of 80 new genes (KIAA0201-KIAA0280) deduced
of cDNA clones from cell line KG-1 and brain.";
3:321-329(1996).
                                                                                                                                                                                                                                                                               IPR003347;
IPR003349;
                                                                                                                     Repeat;
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PubMed=10861003;
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362
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1285
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TF_JmjN.
Znf_C5HC2.
Znf_PHD.
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PHD-TYPE 1.

JMJC:
PHD-TYPE 2.

PHD-TYPE 2.

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V -> L (IN REF. 1).

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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMCY OR HYA.
SMCY OR HYA.
Mus musculus (Mouse).
Mus musculus (Mouse).
Troota; Metazoa; Chordata;
Theria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          062240; Q9QVP9; Q9R040;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                  Burgoyne P.S., Levy E.R., "Spermatogenic failure in Nature 320:170-172(1986).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 23-586 FROM N.A. STRAIN-BALB/c; TISSUE-Testis; MEDLINE-95038738; PubMed-7524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1235
                                                                                                                                                                                                               MEDLINE-95379952; PubMed-7544442; Scott D.M., Ehrmann I.E., Ellis P Simpson E., Mitchell M.J.;
                                                                                                                                                                                                                                                                            Agulnik A.I., Mitchell M.J., Lerner J.L., Woods D.R., Bis "A mouse Y chromosome gene encoded by a region essential spermatogenesis and expression of male-specific minor histocompatibility antigens.", hum. Mol. Genet. 3:873-878(1994).
                                                                                                                                                                                                                                                                                                                                                                                                      SmcY protein (Histocompatibility Y antigen) (H-Y).
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                                                                                                                                      MEDLINE-86146895; PubMed-3951555;
                                                                                                                                                                                                                                                                                                                                                                                            Agulnik A.I., Longepied G., Ty M., "Mouse H-Y encoding Smcy gene and Mamm. Genome 10:926-929(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMCY_MOUSE
                                                                                                                                                     FUNCTION
                                                                                                                                                                            Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                     Identification
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FUNCTION: May play a role in spermatogenesis.

MISCELLANEOUS: SMCY encodes an H-Y epitope that is defined by the octamer peptide TENSGKDI; since no similar peptide was found in SmcX, it is presumably the genetic basis for the antigenic difference between males and females that contributes toward a tissue transplant rejection response.

SIMILARITY: CONTAINS 1 JMJC DOMAIN.
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                                                                                                                                                                           376:695-698(1995).
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1391
1539
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                                                                                                                                                                                                     of a mouse
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1391
A; 174072
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57.00
64.00%
36.00%
35.19%
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male mice lacking
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> G (IN REF. 1).
E58DAE374E3BD7AA
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s X chromosomal homolog Smcx
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                                                                                                                                                                                                                            Bishop C.E., Agulnik A.I.,
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Interpro; IPRO03347; TF_JmjC.
Interpro; IPRO03349; TF_JmjC.
Interpro; IPRO03196; Znf_C5HC2.
Interpro; IPRO011965; Znf_PHD.
Pfam; PF00628; PHD; 4.
Pfam; PF00378; ARID; 2.
Pfam; PF02373; JmjC; 2.
Pfam; PF02375; JmjV; 2.
Pfam; PF02928; zf-C5HC2; 1.
SMART; SM00501; BRIGHT; 1.
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                                                                                                                                               P41230; O9CVI4; O9DOC3; O9OVX8; O9RO39; O5499; O1-FEB-1995 (Rel. 31, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update)
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                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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2 PHD-TYPE ZINC FINGERS.
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IIY -> SFT (IN REF. 2).

F -> S (IN REF. 2).

R -> K (IN REF. 2).

VRTN -> SIWK (IN REF. 2).

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                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Arakawa T. Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ak Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ak Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ak Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ak Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Ak Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Ak Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ak Blake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
Ak Blake J., Boffelli D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
Ak Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
Ak Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
Ak Gustincich S., Hill D., Ringwald M., Rodirjeuez I., Sakamoto N.,
Ak Gustaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ak Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Ak Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Ak Gyrach P., Kontsuki S.,
Ak Gyrach P.,

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                                                                                                                                                                                                                                                                                                           MEDLINE=95379952; PubMed=7544442;
Scott D.M., Ehrmann I.E., Ellis P.S.,
Simpson E., Mitchell M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Jegalian K.G., Page D.C.;
"A proposed path by which genes common to mammalian chromosomes evolve to become X inactivated.";
Nature 394:776-780(1998).
                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                 Simpson E., Mitchell M.J.; \label{eq:model} \mbox{"Identification of a mouse male-specific transplantation antigen}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98389008; PubMed=9723615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawai J., Shinagawa A., Shibata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Embryo, a MEDLINE=21085660; PubMed=11217851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-258
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MEDLINE=95038834; PubMed=7951318;
Wu J. Salido E., Yen P., Mohandas T., Shapiro L.J.
"The murine xel69 gene escapes X-inactivation like
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MEDLINE-99373259; PubMed-10441747;
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"A novel X gene with a widely transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agulnik A.I., Mitchell M.J., Mattei M.-G.,
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                                                                                                                                                                                                                                             Nature 376:695-698(1995).
                                                                                ALTERNATIVE PRÓDUCTS: 2 isoforms; 1 (shown he produced by alternative splicing. MISCELLANEOUS: ESCAPES X:Inactivation. SIMILARITY: CONTAINS 1 ARID DOMAIN. SIMILARITY: CONTAINS 1 JMC DOMAIN. SIMILARITY: CONTAINS 1 JMCN DOMAIN. SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS. SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
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3:879-884(1994).
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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
SmcX protein (Xel69 protein).
SMCX OR XE169.
                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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NCBI_TaxID=9606;
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PROSITE; PS50016; ZF_PHD_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF039894;
MGD; MGI:99781;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zinc-finger;
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                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
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TF_JmjN.
Znf_C5HC2.
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PHO-TYPE 2.

MISSING (IN ISOFORM 2) (BY SIMILARITY).

L -> M (IN REF. 5).

D -> G (IN REF. 5).

D -> N (IN REF. 4; BAB27711).

G -> A (IN REF. 4; BAB277711).
                                                  Craniata; Vertebrata; Euțeleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHD-TYPE 1.
                                                                                                                                                                                                                                                                                                                                                PRT;
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Matches:
Conservative:
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Indels:
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Percent Similarity:
Best Local Similarity:
                                                                                                                                US-09-513-151-3_COPY_1121_1210 (1-90) x SMCX_HUMAN (1-1560)
                                    Query Match:
                                                                                         Pred.
                                                                                                  Alignment Scores:
                                                                                                                            VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                             DOMAIN
ZN_FING
                                                                                                                                                                                                                                           SMART; SM00501; BRIGHT; 1.
SMART; SM00545; JmjN; 1.
SMART; SM00249; PHD; 2.
SMART; SM00249; PHD; 2.
PROSITE; PS01359; ZF_PHD_1; 2.
PROSITE; PS0165; ZF_PHD_2; 1.
                                                                                                                                                                   DOMAIN
ZN_FING
                                                                                                                                                                                                                                                                                                               Pfam; PF02375; jmjN; 1.
Pfam; PF02928; zf-C5HC2; 1.
                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- SIMILARITY: CONTAINS 1 ARID DOMAIN.
-I- SIMILARITY: CONTAINS 1 JMJC DOMAIN.
-I- SIMILARITY: CONTAINS 1 JMJN DOMAIN.
-I- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agulnik A.I., Mitchell M.J., Mattel M.-G., Horsani G., Aviet F.A., Lerner J.L., Bishop C.E.;
"A novel X gene with a widely transcribed Y-linked homologue escapes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-Fibroblast;
MEDLINE-94214434; PubMed-8162017;
MEDLINE-94214434; Salido E., Yen P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wu J., Ellison J., Salido E., Yen P., Mohandas T., Shapiro L.J.; "Isolation and characterization of XE169, a novel human gene that escapes X-inactivation.";
                                                                                                                                                                                                                                 Zinc-finger; Repeat;
                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 314690
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L25270; AAA61302.1; -. EMBL; Z29650; CAA82758.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 levels found in skeletal muscle.
-!- MISCELLANEOUS: Escapes X-inactivation.
                                                                                                                                                                                                                       DOMAIN
                                                                                         Х
..
                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001606; ARID.
InterPro; IPR003347; TF_JmjC.
InterPro; IPR003349; TF_JmjN.
InterPro; IPR004198; Znf_C5HC2.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95038739; PubMed=7951230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 280-344 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                 PF00628; PHD; 2
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                                                                                                                            AA;
                                                                                                                                         184
372
617
1248
1372
342
                                   1.37
57.00
64.00%
36.00%
35.19%
                                                                                                                                                                                                                     ; Alternative splicing
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                                                                                                                           MISSING (IN ISOFORM 2).
C -> Y (IN REF. 2).
W; 78913F010D0BCCE1 CRC64;
                                                                                                                                                                                                          ARID.
                                                                                                                                                                   JMJC.
PHD-TYPE 2.
                                                                                                                                                                                            PHD-TYPE 1.
                                   Conservative: Mismatches: Indels:
                                                                          Length:
Matches:
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                                 Query Match:
DB:
US-09-513-151-3_COPY_1121_1210 (1-90)
                                                                    Best Local Similarity:
                                                                                  Percent Similarity:
                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

MEDLINE-96337999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kalhe B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus Jannaschil.";
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                       Noren C.J., Roberts R.J., Patti J., Byrd D.R., Morgan R.D.;
"Method for screening restriction endonucleases.";
Patent number W09911821, 11-MAR-1999,
-1- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CTAG
AND CLEAVES AFTER C-1 (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
specific double-stranded fragments with terminal 5'-phosphates.
-1- SIMILARITY: STRONG, TO M.THERMOFORMICICUM MTHZIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q58391;
01-NOV-1997
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TIGR; MJ0984;
                                                                                                                                                                                                                                                       EMBL; U67541; AAB98987.1;
                                                                                                                                                                                                                                                                                                        entitles requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Archaea; Euryarchaeota; Methanococci; Methanococcales, Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type II restriction
                                                                                                                                                                                    Complete proteome
                                                                                                                                                                                                    Hydrolase; Endonuclease; Nuclease; Restriction system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-NOV-1997 (Rel. 35, Created)
21-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Type II restriction enzyme MjaI (EC 3.1.21.4)
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                                                                                                                                                                                                                                                                                     send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273:1058-1073(1996).
                                                                                                                                                                                                                                     1221; MjaI.
                                                                                                                                                                      AA;
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                                               .3.52
54.00
72.73%
54.55%
32.93%
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                                                                                                                                                                      9A254A208AB8AC02 CRC64,
x T2M1_METJA (1-222
                               Conservative: Mismatches: Indels: Gaps:
                                                                                                    Matches:
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                                                                                                    12
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ERR2_HU
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                                                                                    SMART;
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095718; 09HCB4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Steroid hormone receptor ERR2 (Estrogen related receptor,
(ERR-beta) (Estrogen receptor-like 2) (ERR beta-2).
DNA_BIND
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 264-500 FROM N.A.

ROWEN L., Madan A., Qin S., Baradarani L., Birditt B., Bloom S.

Dors M., Dickhoff R., Fleetwood P., Harrison G., Kaur A., Madan

Nesbitt R., Traicoff R., Hood L.;

"Sequencing of human chromosome 14q24.3 region.";

Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- SUBUNIT: HOMODIMER (BY SIMILARITY)

-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                    EMBL; AF094517; AAC
EMBL; AC008050; AAG
HSSP; P03372; 1HCQ.
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                    Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00308; STRDHORMONER.
PRINTS; PR00047; STROLDFINGER.
PRODOM; PD0000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bioinformatics and inverse PCR.";
Gene 228:101-109(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen F., Zhang Q., McDonald
Liu Q., Caskey C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                               MIM; 602167;
                                                                                                                                                                                                                                                          TRANSFAC; T02766; -. Genew; HGNC:3473; ESRRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99173874; PubMed=10072763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESRRB OR NR3B2 OR ERRB2.
                                             Receptor; Transcription 
Zinc-finger.
                                                                             PROSITE; PS00031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of two hERR2-related novel nuclear receptors utilizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTGAACCAA
                                                                                                                                                                                                                                                                                                        AF094517; AAC99409.1; AC008050; AAG17472.1;
                                                                                        SM00430; HOLI; 1
SM00399; ZnF_C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
   103
103
139
                                                           NUCLEAR_RECEPTOR; iption regulation;
   168
123
163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T., Davidoff M.J., Bailey W.,
 NUCLEAR RECEPTOR-TYPE C4-TYPE. C4-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                           DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A., Madan
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LeuLysGluLys

63

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RESULT 14
RADC_BACHI
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  US-09-513-151-3_COPY_1121_1210
                                                            Query Match:
                                                                                                                         Score:
                                                                                                                                         Alignment Scores Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                Percent Similarity
                                                                              Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-sentities.
                                                                                                                                                                                                                                  ProDom; PD007415; RadC; 1.
TIGRFAMS; TIGR00608; radc; 1.
PROSITE; PS01302; RADC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
-i- FUNCTION: INVOLVED IN DNA REPAIR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE RADC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20512582: PubMed-11058132:
Takami H., Nakasone K., Takaki Y., Maeno G., S:
Fuji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09K8H4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                            Pfam; PF00633; HHH; 1
                                                                                                                                                                                                                                                                                                                                                     EMBL; AP001517; BAB06751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus halodurans.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RADC OR BH3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADC_BACHD
                                                                                                                                                                                                                                                                                                             InterPro; IPR000445; HhH.
InterPro; IPR001405; RadC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=86665;
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                                                                                                                                                                                                                repair;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysAspLeuAlaAspArgGluLeuValValIleIleGly-----TrpAlaLysHis 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGACCTCTGTGATCGA-----ATCATCATTGGGGATCGCGAATGGGCAGCGCAC
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                                                                                                                                                                                               Complete
232 AA; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                          4.22
53.50
69.57%
47.83%
32.62%
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54.00
57.14%
50.00%
32.93%
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26403 MW;
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  (1-90) x RADC_BACHD (1-232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
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                                                                                                                                                                                               4542153B5C6010D2 CRC64;
                                                          Conservative: Mismatches: Indels:
                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
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Matches:
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Indels:
                                          Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERR2_RAT
p11475;
p11-75;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Steroid hormone receptor ERR2 (Estrogen-related recepta) (Estrogen receptor-like 2).
ESRRB OR NR3B2 OR ESRL2 OR ERR2.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
DNA_BIND
ZN_FING
ZN_FING
SEQUENCE
                                                                                  ProDom; rucconstant 1.

SMART; SM00430; HOLI; 1.

SMART; SM00399; ZnF_C4; 1.

PROSITE; PS00031; NUCLEAR_RECEPTOR;

PROSITE: PROMOSITED TO REGULATION;
                                                                                                                                                                   Pfam; PF00104; hormone_rec; 1.
pfam; PF00105; zf-C4; 1.
PRINTS; PR00308; STRDHORMONER.
PRINTS; PR00047; STROLDFINGER.
ProDom; PD000035; Znf_C4steroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                   EMBL; X51417; CAA35779.1; -. PIR; B29345; B29345.
                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 228:101-109(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen F., Zhang Q., McDonald T., Davidoff M.J., Liu Q., Caskey C.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88122546; PubMed-3267207;
Giguere V., Yang N., Segul P., Evans R.M.;
"Identification of a new class of steroid
Nature 331:91-94(1988).
                                                                                                                                                                                                                                                                      InterPro; IPR001723; Stdhrmn_receptor
InterPro; IPR001628; Znf_C4steroid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bioinformatics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of two hERR2-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                            Receptor; T:
Zinc-finger
                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                 HSSP; P03372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99173874; PubMed=10072763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHOWS THAT REF.1 ORIGINATES FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO ORIGINATE FROM HUMAN BUT WAS LATER SHOWN (REF.2) TO BE DERIVED FROM RAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NR3 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyHisLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACCTCTGTGATCGATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCAAA
                                                                                                                                                                                                                                                                                                             IPR000536; Hormone_rec_lig
    433
                    103
103
139
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  AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: Nuclear (Potential).
BELONGS TO THE NUCLEAR HORMONE
                                        168
123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inverse PCR.";
  48287 MW;
                    C4-TYPE
                                        C4-TYPE.
                                                            NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
  EE2C4C5B2F9A3E13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAT

    DNA-binding; Nuclear protein;

                                                          RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor, beta) (ERR-
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receptors.";

Rattus

receptors utilizing

Bai C.,

FAMILY

and

no 9 its

EMBL outstation

a collaboration

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Alignment Scores:

Pred. No.:

Score:

Score:

Score:

Percent Similarity:

45.83%

Best Local Similarity:

Ouery Match:

1 10

Ouery Match:

1 2.32%

Ouery Match:

1 2.32%

Ouery Match:

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SUMMARIES

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Title:
Perfect score:
Sequence:
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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PN W0200222660-A2.	OS Homo sapiens.	KW expressed sequence tag.	KW neuroprotective; ant	KW antiinfertility; cer	KW Human; antianaemic;	DE Novel human protein SEQ ID NO: 563.		DT 27-JUN-2002 (first entry)	XX	AC ABB97295;	XX	ID ABB97295 standard; Protein; 411 AA.	ABB97295	RESULT 1	
		tag.	<pre>neuroprotective; antiparkinsonian; protein therapy; EST;</pre>	<pre>antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;</pre>	<pre>Human; antianaemic; vulnerary; antiinflammatory; immunomodulator</pre>	SEQ ID NO: 563.		entry)				Protein; 411 AA.			ALIGNMENTS
			py; EST;	rheumatic; gene therapy;	immunomodulator;		-								

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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antianaemic; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopolesis e.g. to treat aplastic anaemia, to help tissue regrowth
                                                                                                                        anticonvulsant; osteopathic; antiarthritic; immunosuppressant; card immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflanmatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                       Human ORFX ORF1724 polypeptide sequence SEQ ID NO:3448.
                                                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                    AAB41960;
                                                                                                                                                                                                                                                                                                                                                                    AAB41960 standard;
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Xue AJ, Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkinson's disease. The present sequence is a protein of the invention
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immunosuppressant; cardiant;
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                                                                                                                                                                                                                                                                                                                                                                                                         antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; humunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cantidabatic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; cantihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating the predistoration associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, or prefit vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, altergies, aplastic anaemia, burns, wounds, bone and cartilage damage, not an activate of the proteins and cartilage damage.
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05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
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                                                                                                                                                                                                                                                                                                                                                                                           nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 2624; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disorders and cardiovascular disease
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                                    AAATCCCACTTGAACCAACTGAAGAAA
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RESULT 3
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ID ABP4

ABP41976 standard;

Protein; 617

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Human; ovarian antigen; ovary; ovarian; breast; cancer; cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; inmune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comperising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of ovarian antigen polynucleofides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitits, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune opphoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders.
                                                                                      respiratory disorders, neurological disorders, gastrointestinal disorders and uninary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forcensic analysis, and the polypeptides may be used as food additives or to prepare antibodies polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding novel ovarian polypeptides useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
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23-AUG-2000; 2000US-0649167
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                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-rell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
sequences (ABLO1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
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2000US-0614150.
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification), ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroldism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
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                                                                                                                                 Disclosure; SEQ:ID 9152; 1037pp; English.
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2000US-228716P
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50.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              frame; ORFX; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; autoimmune thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-90) x ABB65895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cirrhosis;
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US-09-513-151-3_COPY_1121_1210 (1-90) x ABP04585
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. OFFX proteins are also disease and autoimmune inflammatory eye disease.
Molecular identity of the gro-1 gene - useful for cancer diagnosis and/or prognosis, and where compounds affecting encoded proteins as useful for enhancing longevity of a host and inhibiting tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ
                                                                                       WPI; 1999-190615/16.
N-PSDB; AAX36072.
                                                                                                                                                       Barnes
                                                                                                                                                                                                                                                                                                                           04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                   WO9910482-A1
                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gro-l operon; gro-l gene; gop-l gene;
hap-l gene; cancer; aging; longevity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the GRO-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY02526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
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                                                                                                                                                       Η,
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                                                                                                                                                       Lakowski B,
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tumour formation;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
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25-MAR-1999;
29-MAR-1999;
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09-MAR-1999
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                          21-APR-1999
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394 CysGluTleCysAsnTleSerMetThrGlyLysAspAsnTrpGlnLysHisTleAspGly 413
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99US-0128234. 99US-0128714. 99US-0129845. 99US-0130077. 99US-0130449. 99US-0130510.

**S**066 99US-0126785 99US-0126264 9905-0125788 (first entry)

promoter; pathway;

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Best Local Similarity:
                                                                                 Percent Similarity:
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25-FEB-1999

05-MAR-1999

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                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 78196
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                                                                                                                                                                                                                                                                     termination sequence
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990S-0160815

990S-0160980

990S-0160980

990S-0161404

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990S-0161393

990S-0161393
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RESULT 10
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                                                                                               2000EP-0301439
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9905-0121825
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                                                23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                  Drosophila melanogaster.
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(ABB57737-ABB72072).
                        WPI; 2001-656860/75.
N-PSDB; ABL05461.
                                                                                                       23-MAR-2000;
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N-PSDB; ABL02496.
New isolated nucleic acid detection reagent for detecting 1000 or more
                                                                                                                                         23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                             Drosophila melanogaster
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                                                                      New isolated nucleic a
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DB; ABL02386.
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                                                                                                                                                                                                                                                                                                                                                                                                         Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidiabetcl; antiinflammatory; antiulcer; vulnerary; anticonvulsant antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from interactions of the printed specification, but was obtained in electronic format directly from interactions.
New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                 WPI; 2000-611515/58.
N-PSDB; AAF21926.
                                                                                                                                                        Rosen CA,
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antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidiabeterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, altergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAF21614 - AAF22031 represent DNA sequences encoding human proteins AAB58711 - AAB59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences AAF22032 - AAF22040 and AAB59129 which are used in the isolation and characterisation of the DNA and protein sequences of the
                                                                                                                                                                                                                                                                                                                                                            or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic;
Sequence
                                                    cerebral anoxia and epilepsy; and infectious
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                                                                                                                                                                                                                                                                                                                                                                                                                invention. The breast and ovarian cancer associated DNA, protein, agonist
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US-09-513-151-3_COPY_1121_1210 (1-90) x AAB59023 (1-737)

Best Local Query Match: Percent Similarity: Similarity: 2.07 57.00 53.57% 39.29% 34.76% 21 Mismatches: Indels: Conservative: 0 0 13

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Вb ρ 47 CysGluLeuCysAspValSerCysThrGlyAlaAspAlaTyrAlaAlaHisIleArgGly 66 TGTGACCTCTGTGATCGATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCC 60

Š 61 AAATCCCACTTGAACCAACTGAAG 84

В 67 AlaLysHisGlnLysValValLys

Search completed: April 21, Job time: 5.16753 secs 2003, 18:48:18

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-Q-ggp2__I/USPTO_Spool_VG09513151/runat_15042003_141145_26452/app_guery.fasta_1.2446
-DB-Pending_Patents_AA_New -OFMT-fastan -SUFFIX-n2p.rapn -MINMATCH-0.1
-LOOPEXY-0 -UNITS-Dits -STARY-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALIGN-200 -THR_KCORE-pct -THR_MXX-100
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-NCPU-6 -ICPU-3 -NO_XLDXY -NO_MMAP -LARGEQUERY -NGS_SCORES-0 -MAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPON-10 -XGAPEXT-0.5 -FGAPOP-6
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; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS
; FILE REFERENCE: 21272-114
; CURRENT APPLICATION NUMBER: U$/10/380,7
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 09/659,671
; PRIOR FILING DATE: 2000-09-11
; NUMBER OF SEQ ID NOS: 888
; SOFTWARE: Custom
; SEQ ID NO 563
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           CATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAGGGA 898
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RESULT 4
US-60-453-135-7967
| Sequence 7967, Application US/60453135
| GENERAL INFORMATION:
| APPLICANT: CARGILL, Michele
| APPLICANT: CARGILL, Michele
| APPLICANT: CARGILLA, Oldan
| APPLICANT: TAKOUBOVA, Oldan
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S-60-453-135-7967
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CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
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TITLE OF INVENTION: MYCCARDIAL INFARCTION, METHODS OF DETTITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-03-10 NUMBER OF SEQ ID NOS: 82762
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                                                                                                                                                                                                                                    TITLE OF INVENTION: GENETIC POLYMORPHISMS TITLE OF INVENTION: STENOSIS, METHODS OF FILE REFERENCE: CL001457
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                                                                                                                                                                 TYPE: PRT
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US-60-453-135-7969
; Sequence 7969, Application US/60453135
; GENERAL INFORMATION:
                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-513-151-3 (1-2041) x US-60-453-135-7969
                                                                                               Alignment Scores:
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CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7969
LENGTH: 85
                                                                                                                                                                                                                                              APPLICANT: CARGILL, Michele
APPLICANT: IAKOUBOVA, Olga.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                  TYPE: PRT
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RESULT 8
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LENGTH: 85
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APPLICANT: CARGILL, Michele
APPLICANT: LUKE, May
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CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
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PCT-US02-36123-4332
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Best Local Similarity:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 4332
LENGTH; 315
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TITLE OF INVENTION: Allolococcus ottitidis Open Reading Frames (ORFs) Encoding Polyper TITLE OF INVENTION: Antigens, Immunogenic Compositions and Uses Thereof FILE REFERENCE: Application 1
CURRENT APPLICATION NUMBER: PCT/US02/36123
CURRENT FILING DATE: 2003-01-02
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                ArgValAspGlnMetValAspLysGlyLeuLeuGluGluVal---
                                                                                GlnAlaPheIleIleGlyLeuAsnThrAspArgSerLysLeuTyrAspArgIleAsnThr
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APPLICANT: George H. Miller
APPLICANT: Roberta S. Hare
APPLICANT: Karen J. Shaw
TITLE OF INVENTION: Staphylococcus aureus Re.
FILE REFERENCE: 1034/1C963US2
CURRENT APPLICATION NUMBER: US/09/950,084
CURRENT APPLICATION NUMBER: US 09/417,811
PRIOR APPLICATION NUMBER: US 09/417,811
PRIOR FILING DATE: 1999-10-14
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,556
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,555
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR APPLICATION NUMBER: US 09/266,542
PRIOR FILING DATE: 1999-03-11
US-09-513-151-3 (1-2041) x US-09-950-084-4328 (1-319)
                                                                                     Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                   ; ORGANISM: Staphylococcus
US-09-950-084-4328
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                                                                                                                                  Score:
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; SEQ ID NO 4328
; LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/036,720 PRIOR FILING DATE: 1998-03-06 PRIOR APPLICATION NUMBER: US 09/036,338 PRIOR FILING DATE: 1998-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-03-11
PRIOR APPLICATION NUMBER: US 09/037,934
PRIOR FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                             Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 7451
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                                                                                                                                                                                                                                                              TYPE:
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Gaps:
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Conservative:
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US-10-289-762-983
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          Alignment Scores
                                      ; ORGANISM: Chlamydia
US-10-289-762-983
                                                                                      TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999 CURRENT APPLICATION NUMBER: US/10/289,762 CURRENT FILING DATE: 2003-03-27 NUMBER OF SEQ ID NOS: 6849 SEQ ID NO 983
                                                                                                                                                                                            Sequence 983, Application US/10289762
GENERAL INFORMATION:
APPLICANT: Griffais, R.
                                                               LENGTH: 34
TYPE: PRT
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TyrIleGlnSerLeuIleTyrAsnTyrGluLeuGluAspGluThrValThrProAlaGln 134
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-----GinGinLeuValGluGinGlyTyrGluSerCysGinSer-----MetGin
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31.65%
8.94%
Gaps:
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Indels:
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Conservative:
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US-09-513-151-3 (1-2041) x US-10-289-762-983 (1-342)
Sequence 4171, Application US/10092411A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-101
CURRENT APPLICATION NUMBER: US/10/092,411A
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: US 09/134,001
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5676
                                                                                                                                                         Sequence 4383, Appli
GENERAL INFORMATION:
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                                                                                                                                                                                               -09-134-000C-4383
             CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 198-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15
                                                                                     APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO TITLE OF INVENTION: ENTERCOCOCCUS FAECALIS FILE REFERENCE: 032796-032
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ID NOS: 6812
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LENGTH: 311
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                                               CAACATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATCACTGAG
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US-09-513-151-3 (1-2041) x US-09-134-000C-4383 (1-311)
                           Conservative:
Mismatches:
Indels:
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Matches:
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 4383
LENGTH: 311
TYPE: PRT
ORGANISM: Enterococcus faecalis
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 03796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
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                                   GGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTT 655
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               ; TYPE: PRT; ORGANISM: Propioni acnes PCT-US02-32727-18388
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                                                          CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
SEQ ID NO 18388
LENGTH: 357
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                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                     APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: 210121.514C1
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Jones, Robert
Carter, Darrick
Barth, Brenda
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|Leu 295
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                                                                                                                                                                                                               GAGGAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAG
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-Q-/G9D2_1/USPTO.Spool/US0953151/runat_15042003_141145_26426/app_query.fasta_1.2446
-Q-/G9D2_1/USPTO.Spool/US0953151/runat_15042003_141145_26426/app_query.fasta_1.2446
-DB=Pending_Patents_AA_Main -QFMT=fastan -SURFIX=n2p.rapm -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09513151_@CGN, 11_422_@runat_15042003_141145_26426
-NCPU=6 -LOPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Fgapop 6.0,
Delop 6.0,
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/cgn2_6/ptodata/1/paa/US06_COMB.pep:*
/cgn2_6/ptodata/1/paa/US07_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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## ALIGNMENTS

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PRIOR APPLICATION NUMBER: 60/276,026	PRIOR FILING DATE: 2001-09-27	PRIOR APPLICATION NUMBER: 60/325,149	PRIOR FILING DATE: 2001-03-14	PRIOR APPLICATION NUMBER: 60/276,025	CURRENT FILING DATE: 2002-03-14	CURRENT APPLICATION NUMBER: PCT/US02/07826	FILE REFERENCE: MRI-030PC	TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer	TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,	APPLICANT: Millennium Pharmaceuticals, Inc. et al.	GENERAL INFORMATION:	; Sequence 153, Application PC/TUS0207826	PCT-US02-07826-153	RESULT 1

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PRIOR APPLICATE: 2001-0-19
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
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OR APPLICATION NUMBER: 60/324,967
OR FILING DATE: 2001/09/26
OR FILING DATE: 2001-09-10
OR APPLICATION NUMBER: 60/311,732
OR APPLICATION NUMBER: 60/325,102
OR APPLICATION NUMBER: 60/325,102
OR APPLICATION NUMBER: 60/323,580
OR APPLICATION NUMBER: 60/323,580
OR FILING DATE: 2001-09-19
BER OF SEQ ID NOS: 363
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                                          APPLICANT: John MONAHAN
APPLICANT: Manjula GANNA
APPLICANT: Sebastian HOE
APPLICANT: Sebastian HOE
APPLICANT: Sceve G. KOVA
APPLICANT: Steve G. KOVA
APPLICANT: Rachel E. MEY
APPLICANT: Michael MORRI
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Robert C. BAS
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ICANT: Xume1 ZHAO
ICANT: Karen GLATT
E OF INVENTION: Nucleic Acid
E OF INVENTION: Assessment,
REFERENCE: MRI-030
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Rachel E. MEYERS
Michael MORRISEY
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Shubhangi KAMATKAR
                                             Rosemarie SCHMANDT
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PRIOR APPLICATION NUMBER: 00/109-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows V.
SEQ ID NO 153
LENGTH: 467
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-097-340-153
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PRIOR FILLING DATE: 2001-09-26
PRIOR FILLING DATE: 2001-09-26
PRIOR FILLING DATE: 80/276,026
PRIOR FILLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILLING DATE: 2001/09/26
PRIOR FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILLING DATE: 2001-09-26
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RESULT 3

PCT-US02-07826-151

Sequence 151, Application PC/TUS0207826

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et
TITLE OF INVENTION: Massessment, Prevention, ar
TITLE OF INVENTION: Assessment, Prevention, ar
TITLE OF INVENTION: Assessment, Prevention, ar
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CURRENT APPLICATION NUMBER: PCT/US02/07826
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
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PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,580
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOPTWARE: FRSTSEQ for Windows Version 4.
SEQ ID NO 151
LENGTH: 465
TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 151, Application US/10097340 Sequence 151, Applicant	3 CANGAGCTGAAATGCAGCGTT 1333 	3 AGTGTTTCCCCAGACTATAACAAAGAACCTAAAAGGAAGG	3 AACCAACTGAAGAAAGAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAG 1252 	33 GATCGAATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTG 1192 	3 ATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGACCTCTGT 1132 	3 GAACCTGCTCTGAAATCGTGCAAAGTTTCATCCAGGGCCACAAGCCTACAGCCACTCCA 1072	33 GTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTT 1012 	1CTGGTCCCATT 952 		_CAATCAATTGGCTTCAAGGAATTTCAGGAGTACCTGATCACTGAGGAAAATGCACACTG	9 1	GATAAGAGGGTGGATGACATGCTTGCTGCTCTTGGAGGAACTAAGAGATTTTCAC 

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PRIOR FILING DATE: 2001/09/20
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 5EQ ID NO 151
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PRIOR APPLICATION NUMBER: 60/276,025
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PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
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APPLICATION NUMBER: 60/
FILING DATE: 2001/09/26
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RESULT 5
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; Sequence 1394, Application PC/TUS0101239
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, at
; ETLE REFERENCE: PT213PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01239
; CURRENT FILING DATE: 2001-01-17
; CURRENT FILING DATE: 2001-01-17
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RESULT 6
PCT-US01-01349-586
PCT-US01-01349-586
; Sequence 586, Application PC/TUS0101349
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc., et al
; TITLE OF INVENTION: Nucleic Acids, Proteins,
; FILE REFERENCE: PJZ06PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01349
; CURRENT FILING DATE: 2001-01-14
; Prior application data removed - consult PALM
; NUMBER OF SEQ ID NOS: 939
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; LOCATION: (124)
; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (145)
; OTHER INFORMATION: X
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic FILE REFERENCE: PJZ06
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SEQ ID NO 586
LENGTH: 222
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CURRENT FILING DATE: 2001-01-17
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Sequence 784, Application US/09764853
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Ant
FILE REFERENCE: PJ206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or fil
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (145)
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TYPE: PRT
ORGANISM: Homo sapiens
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; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (145)
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PTZ13
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SEQ ID NO 1394
LENGTH: 222
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ORGANISM: Homo
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Sequence 586, Application US/10072326

GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic acids, Proteins,
FILE REFERENCE: PJZ06C1
CURRENT APPLICATION NUMBER: US/10/072,326
CURRENT FILING DATE: 2002-02-11.
Prior Application removed - See File wrapper
NUMBER OF SEQ ID NOS: 939
SOCTWARE: Patentin Ver. 3.1
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OTHER INFORMATION: Xaa e NAME/KEY: misc_feature LOCATION: (145)
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CURRENT FILING DATE: 2002-02-11.
Prior Application removed - See File wrap:
NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 784
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06C1
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TYPE: PRT
ORGANISM: Homo sapiens
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SEQ ID NO 2199
LENGTH: 143
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CURRENT FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM001
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                                         HisProHisAspLysArgLysValAlaArgSerLeuGlnValPheGluGluThrGlyIle
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CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 09/757,028.
PRIOR FILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR PPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 2660
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PM001C1N
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Sequence 44570, Application US/09270767
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

LENGTH: 252

TYPE: PRT
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665 CTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAG 724
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-Q-/cgn2_1/USPTO_Spool/US09513151/runat_15042003_141144_26406/app_query.fasta_1.2446
-DB-ISSued_Patents_AA -QFMT=fastan -SUFFIX=nDp.ra1 -MINNATCH=0.1 -LOOPCL=0
-LOOPCL=0 -UNITS-Shits -START=1 -END-1 -MATRIX-blosum62 -TRANS-bluman40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -QUTFWT-pto -NORM-ext -HEAPSIZE-500 -MINLEN=0 -MAXLEN=2000000000
-USER-US09513151_@CGN_1_1_20#-mnat_1504003_141144_26406 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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GENERAL INFORMATION:

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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4171
LENGTH: 193
TYPE: PRT
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Best Local Similarity:
Query Match:
                                                                            US-09-513-151-3 (1-2041) x US-09-134-001C-4171 (1-193)
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                                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
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322TyrGlyLysAspIleThrGluLeuIleAlaTyrGlnSerLysLeu 336	da	-09-513-151-3 /1-20/1\ \tau_{100-124-00-124} \ \tau_{100-124-00-124-00-124} \ \tau_{100-124-00-124-00-124} \ \tau_{100-124-00-124-00-124} \ \tau_{100-124-00-124-00-124-00-124} \ \tau_{100-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-00-124-0
953 GTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGGAGGAGTCTGTTCTT 1012	Qy .	Match: 3.20% Indels:
307 GluTyrGluSerArgMetAsnLeuLeuAsnAsnLeuLysArgLys 321	Db	20.04% Conservative:
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773 GAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGAC 832	Qy	NUMBER OF SEQ ID NOS: 5674
265 IleValProGluLysPheValArg	dd	PRIOR APPLICATION NUMBER: US 60/055,779
713 GTTCTAGATGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCT	Qy	; PRIOR APPLICATION NUMBER: US 60/064,964 ; PRIOR FILING DATE: 1997-11-08
250AspArgLeuTyrGluLeuSerAsnTyrLeuGlnThrIleAsnAsp 264	Db	CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
653 CTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAGGCA 712	Qy	S FOR DIAGNOSTICS AND THERAPEUTICS
230 LysLeuAsnLeuAlaLeuAsnAsnAlaHisGlnValLeuThrAspGluSerAlaIlePro 249	DCOCCUS	; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
614 TITCTC		; Patent No. 6380370 ; GENERAL INFORMATION:
215 ValAspGlnLeuGluSerAspIleLysArgIleGlnAsnSerGlu 229	Db	US-09-134-001C-3172 ; Sequence 3172, Application US/09134001C
554 AAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAA 613	Qy	RESULT 2
195 LeuAspLeuMetLysPheGlnLeuGluGluLeuThrGluAlaSerLeuLysGluGlyGlu 214	Db	Db 162 HisProAsnArgLysArgValLeuArgAlaIleGluTyrTyrLeuLysThr 179
_	γQ	Qy 542 CATCCACATGACAAACGCAAAGTGGCCCAGGAGCTTGCCAAGTTTTTGAAGAAACA 595
LysasnLysargLysGluLeuGluGluLeuGluSerAlaAspGlnAlaLeuLeuGlnArg	Db	Db 142 AsnAsnAsnLysLeuHisGluTyrLeuAlaSerPheAspLysGluSerAlaLysAspIle 161
ATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTTCACAAACGC	QY	TGGTCTTGTACTTCACAAACGCCTAAGCCAGGTG
/ AspasnGinTyrSerAspLeuLeuAsnGinTyrGinLeuSerTyrAsnGinTyr	טט	Db 122 SerIleSerGluAspLysMetLysGlnValLysLeuLysLeuLysGluLeuGluHisLeu 141
CTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAGAAAGTG	Qy	Qy 425 CCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAG 481
GIUTHIGINSETLEULEULYSGIHLYSTYTHISLEUGIHLEULEUASPASPTYTALA	טט	Db 102 AlaGlyGlyThrGlyLeuTyrIleGlnSerLeuLeuTyrAsnTyrAlaPheGluAspGlu 121
AAAATTCCTATTGTTGTGGGAGGAACCAATTATTACATTGAATCTCTG	2, QY	Qy 365 GTGGGAGGAACCAATTATTACATTGAATCTCTGGCTCTGGAAAGTTCTTGTCAATACCAAG 424
ThrLeuGinAspLeuArgLysVaiMetGinGluLeuLeuAspIleHisGlyGlnHis	Db	Db 82 LysLysArgAlaGluLysTyrIleLysAspIleThrArgArgGlyLysValProIleIle 101
ACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGAC	Qy	Qy 305 AGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGACAAAATTCCTATTGTT 364
	Db	Db 63 ProHisTyrMetIleAspIleLeuProProAspAlaSerPheSerAlaTyrGluPhe 81
	Qy	QY 245 CGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTC 304
89 AlaIleAspValAspGluAspPheLeuLeuValLysArgGluIlePheSerSerGlyLys 108	Дb	
	Qy	QY 185 GTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTCTGCCCCAAGAGCAGAGAATCTGC 244
69 IleGluGlyIlePheAspIleAspGluSerLysAspAlaIleAsnIleLeuGluSerLeu 88	Дb	
	_	QY 125 CTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAG 184

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CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gotthardt, Michael TITLE OF INVENTION: LDL Receptor Signaling FILE REFERENCE: UTSW0708
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LeuAsnLeuLeuTyrValGlnAlaGlyAspAspIleLeuAsnGlySerHisProHisSer 231
                                                                         LeuLeuArgArgLysPhePheTyrGluAspGlnAsnValAspSerArgAspProPheGln
                                                                                                                                                   AsnTrpLeuAspHisGlyArgThrAlaArgGluGlnGlyValGluGluHisGluAspLeu
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                                    CTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGT-----CCTCTGAAG
                                                                                                              AAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08463092B Patent No. 5766880
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                    SOFTWARE: ASCII text CURRENT APPLICATION DATA:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1232
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                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Cole, Susan P.C.
APPLICANT: Deeley, Roger G.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1268 TATAACAAAGAACCTAAA 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 GAACCTGCTCTTGAAATCGTGCAAAGTTTC-----ATCCAGGGCCACAAGCCTACAGCC 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 PheAspLysAlaCysGluPheAlaIlePheGlnCysGlnIleGlnPheGlyProLysAsn
                                                            OPERATING SYSTEM:
                                                                                                                                                    ZIP: K7L 3N6
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                          CITY: Kingston
STATE: Ontario
                                                                                                                                                                                                                                     STREET:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluSerThrMetLysGluAspSerValSerProLysLysSerLeuValLeuGlnGlnGln 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysLysLysSer-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTCCAATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAAGTTATCACCTGTGTGAC 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValProArgLeuTrpGlyIleThrLysGluCysValMetArgTyrAspGluLys-----
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                                                                                                                                                                                                                                     E: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS Queen's University at Kingston
                                                                                                                                                                           CANADA
                                                               PC-DOS/MS-DOS
US/08/463,092B
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131 TTGCAGCTAGGCCAGCGGCTGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTAT	US-09-513-151-3 (1-2041) x US-08-463-092B-7 (1-1548)  Qy	Alignment Scores: 0.12 Length: 1548 Score: 99.00 Matches: 74 Percent Similarity: 36.638 Conservative: 52 Best Local Similarity: 21.518 Mismatches: 88 Query Match: 2.778 Indels: 130 DB: Gaps: 19	TRATION WE WOULD SEND TO THE T	FILING DATE: 05-JUN-1995  CLASSIFICATION: 435  PRIOR APPLICATION UNMBER: 07/966,923  FILING DATE: 27-OCT-1992  CLASSIFICATION UNMBER: 08/029,340  FILING DATE: 8-MAR-1993  CLASSIFICATION UNMBER: 08/029,340  FILING DATE: 8-MAR-1993  CLASSIFICATION UNMBER: 08/141,893  FILING DATE: 26-OCT-1993  CLASSIFICATION DATA:  APPLICATION UNMBER: 08/141,893  FILING DATE: 26-OCT-1993  CLASSIFICATION UNMBER: 08/407,207  FILING DATE: 20-MAR-1995  CLASSIFICATION UNMBER: 08/407,207  FILING DATE: 20-MAR-1995  CLASSIFICATION: 435  PRIOR APPLICATION UNMBER: 08/407,207  FILING DATE: 20-MAR-1995  CLASSIFICATION: 435  ATTORNEY/AGENT INFORMATION:
een's University at Kingston gton ario ANADA  ARBLE FORM: ABLE FORM: COMPATIBLE PC-DOS/MS-DOS ASCII text CATION DATA: NUMBER: US/08/460,907B  10N: 424 TION DATA: NUMBER: 07/966,923 1: 27-0CT-1992 ION: 424	SULT 5  -08-460-907B-7  -08-460-907B-7  Sequence 7, Application US/084609  Sequence 7, Application US/084609  Sequence 7, Application US/084609  GENERAL INFORMATION:  APPLICANT: Deeley, Roger G.  APPLICANT: Cole, Susan P.C.  TITLE OF INVENTION: METHODS I  TITLE OF INVENTION: RESISTAND  NUMBER OF SEQUENCES: 9  CORRESPONDENCE ADDRESS:  ADDRESSEE: PARTEO RESPARCH  ADDRESSEE: ADRESS	Ate 111 299 119	1471SeralaTyrThrVallleThrIleAlaHisArgLeuHisThrVall 647 GGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGAC 1485	1397 GluLeuValGlyLeuArgGluArgValAlaSerGluSerGluGlyIleAspSerArg

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TELEFAX: (613) 545-6853
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1548 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Steeg, Carol Miernick1
REGISTRATION NUMBER: 39,539
REFERENCE/DOCKET NUMBER: 01551
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1271 AlaGlyAlaAlaSerSerAlaLeuHisProValGlnAlaGlySerLeuValLeuGluGly 1290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/407,207
FILING DATE: 20-MAR-1995
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APPLICATION NUMBER:
FILING DATE: 26-0CT-
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                                                                                                                                                                                 1377 ValArgGlnAsnValAspProPheLeuGluAlaSerSerAlaGluValTrpAlaAlaLeu 1396
                                                                                                                                                                                                                                                                       1358 GluLeuArgArgHis---PheSerMetIleProGlnAspProValLeuPheAspGlyThr 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 TIGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTAT 190
                                          350 AAAATTCCTATTGTTGTGGGAGGAACCAATTATTACATTGAATCTCTGCTCTGGAAAGTT 409
                                                                                                                                    296 -----GTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGCCCGAGAC 349
                                                                                                                                                                                                                                 293 GTG------
                                                                                                                                                                                                                                                                                                                      239 ATCTGCCGGCACCACATGATCAGCTTTGTG-----GATCCTCTTGTGACCAATTACACA 292
                                                                                                                                                                                                                                                                                                                                                                                                              191 GAA-----GGCCTAGACATCATCACCAAC-----AAGGTTTCTGCCCAAGAGCAGAGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 -----ATTCTCGGGGCCACGGCAAATCCACGCTGGCG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 CTGCAA------CGGACCCTACCTCTTGTAGTG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
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----ValLeuGluGlyGlySerAsnTyrSerVal---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-0CT-1993
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2.77%
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88
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NFORI	TELL R	ATTC	₹≥	CURI	203	COM	4 C S	C 83	CORI	TITLE	APPI	ENER	SULT 6 -08-777-40 Sequence 2 Patent No.	1533	878	1513	827	1499	767	1486	707	1485	647	1471	587	1458	527	1438	470	1426	410
TELEFAX: (312) 474-0448 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	TELEPHONE: (312) 474-6300	4.55 FORMATI 753and, MBER:	APPLICATION NUMBER: US/08/777,405A FILING DATE:		IBI	三日	STATE: Illinois SCUNTRY: USA ZID: 60606	300 Sears Tower/233 South Wacker Driv cago	PONDENCE ADDRESS: PONDENCE ADDRESS: PONDENCE ADDRESS:	OF INV	Hoekstra, Merl F. Holtzman, Douglas	NFOR	ULT 6 Requence 2, Application US/08777405A Retent No. 5858753	GluLeuLeuMet 1536				ValAlaGluMetGlySerProArgGluLeuValMetAsnHis 151	TTGGAGGAACTAAGAGATTTTCACAGACGCT	AlaGlnTyrAspLysIleIleValMetAspHisGlyVal 149	CAGGCAGTTCTAGATGAGGCGTTGGATAAGAGGGTGGATGACATGCTTGCT	148	GGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTT	Гег	GAAGAACAGGAATCTCTCATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGTGGT 646	LeuAspArgGlnIleGlnAlaThrValMetSerAlaPhe 1470	. 🔄			GlyGlnArgGlnLeuMetCysMetAlaArgAlaLe	

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                             heGlnTyrIleCysSerCysLeuHisSerGlyLeuThrProHis-----LeuThrMetV 277
                                                              TCAAGGAA-----TTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGG 911
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERRISTICS:
LENGTH: 1044 amino acid:
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RESULT 8 US-09-225-9 US-09-225-9 Sequence Patent NA GENERAL APPLIC APPLIC APPLIC ITITE UMBEE CORRES CORRES CORRES CONT STR CITY STR COUD COUD COUD COUD COUD APPLIC	4 0	1385	1329	40	γ c	1209	371	1149	352	1113	்	317	996	297	956	277	912	259
JULT 8 309-225-951-2 squence 2, Application US/09225951 stent No. 598589 stent No. 598589 applICANT: Chantry, David APPLICANT: Hockstra, Merl F. APPLICANT: HOLTZMAN, Douglas A TITLE OF INVENTION: No. 5985589el Lipid Kinase NUMBER OF SEQUENCES: 17 CARRESPONDENCE ADDRESS: ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun STREET: 6300 Sears Tower/233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/09/225,951 FILING DATE: CLASSIFICATION: AMBE: NO. 5985589and, Greta E. REGISTRATION NUMBER: 35,302	nLeuLysThrGlyGluArgCysLeuTyrMetTrp	адалярсуветоттельнаттрынальныеспеченыныхртутыужларь чэт	;	413	TANCAAAAAACTAACCTAAAACCCAAACCCATCACCCCACAAATCAATCAACAA	GAAGAAGATTGGACTCAGATGCTGTCAACACCATAGAAAGTCAGAGTGTTTCCCCAGACT 1268          -	::::::      :::         :::	GGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTGAACCAACTGAAGAAAA 1208	etLeuCysLysThrValSerSerSerGluValSerValCysSerGluProVal 370	2 cs. susakirostandandandandungan	TCCAATAAAGATGCCATACAATGAAGCTGAGAACAAGAGAGAAGTT 11	GlnProPheArgIleGluLeuIl	GGGAGGAGTCTGTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACA 1055	::: :::            117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117    117	TCTATGGCTTAGAGGTATCTGATGTCT	alHisSerSerIeLeuAlaMetArgAspGluGlnSerAsnProAlaProGlnValG 297	AGACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTC- 955	TCAAGGAATTTCACGAGTACCTGATCACTGAGGAAAATGCACACTGG 911     :

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 27866/33441

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1044 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                          720
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                                                                                                           heGlnValSerThrLysAspValProLeuAlaLeuMetAlaCysAlaLeuArgLysLysA 225
                                                                                                                                                                                                                                                                                                            ysGluGluAlaAlaAlaArgArgGlnGlnLeuGlyTrpGluAlaTrpLeuGlnTyrSerP 167
                                                                                                                                                                                                                                                                                                                                                                         luPheAspSerLeuCysAspProGluValAsnAspPheArgAlaLysMetCysGlnPheC 147
                                                                                                                                              ATGAGCGCTTGGATAAGAGGGTGGATGACATGCTTGCTGCT---------
                                                                                                                                                                             euProAsnArgAlaLeuLeuValAsnValLysPheGluGlySerGluGluSerPheThrp 205
                                                                                                                                                                                                           TCTCTAACCCTTGCATCCTT-----TGGCTTCATGCTGACCAGGCAGTTCTAG 719
                                                                                                                                                                                                                                          heProLeuGlnLeuGluProSerAlaGlnThrTrpGlyPro-----GlyThrLeuArgL 185
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	201A-2 2, Application US/09019201A 0. 5968780 1 NOROMATION: 1 NORMATION: 1 NORMATION: 1 NORMATION: 1 LI, YI CANT: SOPPET, DANIEL R. CANT: DILLON, PATRICK J. 0 F INVENTION: 0 DENDRITIC CELL-DERIVED GROWTH R OF SEQUENCES: 11 SPONDENCE ADDRESS: 1 SPONDENCE ADDRESS: 1 SPONDENCE ADDRESS: 1 RESEE: HUMAN GENOME SCIENCES, INC. EET: 9410 KEY WEST AVENUE Y: ROCKVILLE TER READABLE FORM: 1 20850 TER READABLE FORM: 1 10M TYPE: Floppy disk PUTTER: IBM PC Compatible PUTTER: IBM PC Compatible PUTTER: IBM PC COMPATIBLE THANKE: PATENTIN Release #1.0, Version #1.30 NT APPLICATION DATA: 1 130 NT APPLICATION DATA: 1 130 NT APPLICATION NUMBER: US/09/019,201A SSIFICATION: 536	AGGGAGGGGTATGTTTGTCTCCCAGTCTGG :::	GCGTTTAAGAGACATGTCCAGTGGCCTTTGGAAAGGTGGTGGGGATCCAGTTCAGG	:::     hrLysLysSerLysLys	echtaafgheucysphealaleuryfalavalileglubysalabysbysalaafgserr ATAACAAAGAACCTAAAGGGAAGGGATCCCCAGGGCAGAATGATCAAGAGCTGAAATGCA		GGGATCGCGAATGGGCAGCACATAAAATCCAAATCCCACTTGAACCAACTGAAGAAAA 1208     :::::       :::::         :::::::::	GACCTCTGTGATCGAATCATCATTG :::    erGluValSerValCysSerGluProVal			GAGTCTGTTCATGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAGGGCCACA 10		1HisSerSerTleLeuAlaMetArgAspGluGlnSerAsnProAlaProGlnValG 29	AAGAAAGGACCTGGTCCCATTGTC-	SerCysLeuHisSerGlyLeuThrProHis		

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NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF346
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TO NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
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SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acidi
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  229 PheArgSerMetGlnGluPheTyrGlu-----
                                                                                                                      854 TCAATTGGCTTC-----
                                                                                                                                                         189 ValThrGlnHisProGluValIleTyrThrAsnGlnAsnValValTrpSerLysPheGlu 208
                                                                                                                                                                                                 794
                                                                                                                                                                                                                                      176 ThrGluPheAspAspSerLeu-------LeuArgAsnPheThrLeu 188
                                                                                                                                                                                                                                                                                                                  162 Trp----
                                                                                                                                                                                                                                                                                                                                                           692 TGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGCTTGGATAAGAGGGTG------ 742
                                                                                                                                                                                                                                                                                                                                                                                               142 GlyIleMetGlnPheArgPheAlaHisProThrProArgProSerGluLysCysSerLys 161
                                                                                                                                                                                                                                                                                                                                                                                                                                      656 GGA---GGTCCTCTGAAGTTCTCTAACCCT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      491 GTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCA--- 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GlySerAlaLeuSerTleAspGluThrArgAlaHisLeuLeuLysGluLysMetMet 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 SerMetH1sPhePheGlnAlaLysH1sLeuIleGluArgSer---GlnValPheAsnIle 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ThrLeu-----LysIleAlaGluMetLysGluAlaMetArgThrLeuIlePheProPro 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 ArgLeuGlyGlyArgLeuValLeuAsnThrLysGluGluLeuAlaAsnGluArgLeuMet 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                        ------AAGGAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAG 913
                                                                             ThrIlePhePheThrIleSerGlyLeuIleHisTyrAlaProValPheArgAspTyrVal 228
                                                                                                                                                                                               CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA 853
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----AspAsnValLeuTyrMetGlu 244
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9-513- 32 97 62 117 112 136 136 156		-3100 and the control of the control	1154 307	1094 293	1034 274	974 254	914 245
CGAGCAGTTC CGAGCAGTTC	Scor     mila   Sim   Ch:		CGCGA :    tAlan	GCTGA	CAAAG     GlnLy	GAGGT	ACTAG IleAr
CGAGCAGTTCCTGTGGGCAGT	es: rity: illarity	363C-6 363C-6 10	CGCGAATGGGCAGCGC :        tAlaMetGlyLeuArg	GCTGAGAACAAGAGAAGTTATC    :::::::    His-ArgSerLysAspVal	AAAGTTTCATCCAGGGCCACAAGCCTACAGGCCACTCCAATAAAGATGCCATACAATGAA       ::::::              nlyspheValGluthtHisProGlupheIleGlyIleLysIleIleTyrSerAsp	GAGGTATCTGATGTCTCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTG     ::         SerGlyGluHisHisAspGluGluTrpSerValLysThrTyrGlnGluValAla	ACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCCCCTGTCTATGGCTTA :::        !!##########################
2041) CCTGTG        Proval' Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'   Proval'		lication li69 li710N: pra li, Jinrui j. Jinrui	CAGCG(	AGAGAJ ::::: Lysası	TCCAGO ::::: alGlu	ATGTC: lyGlu	AGCTTCTA ::      rgLeuLeu
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41) x US-09-310-363C-6 (1-430)  TGTGGGCAGT	)	use 10, 9	•	ACCTGTGTGACCTCTGTGATCGATCATCATTGGGGAT :::         :::  AlaValIleAlaGluSerIleArgMe	CCTACAGCCACTCCAATAAAGATGCCATACAATGAA 	GGAGTC       GluTr	ACCTGG
363C-6 (1-430)  SerPheAlaLeuAspMetAlaLeuGlyThrGly SerPheAlaLeuAspMetAlaLeuGlyThrGly GTGATTCTCGGGGCCACGGCACACGGCACATCC GIUVAITyrGlyProGluAlaSerGlyLySThr GGCCAGGGGCGGGGGGGGGAGATCGTCAGCGGT    :::       AlaGlnLysAsnGlyGlyTyrCysAlaPheVal AlaGlnLysAsnGlyGlyTyrCysAlaPheVal GTCTATGAAGGCCTAGACATCATCACCAACAAG :::     LeuAlaGluSerIleGlyValAspThrAsnAsn	th: hes: erva erch	ss Thereof		CCTCT	CACTO	rgrrc	TCCCA
euAspM euAspM liggGCCA   	tive:	eo f		GTGATO	CAATAA        yilei	TTGAAC ::::: hlLysT	rTGTCC
fetAla (CGGGC (CGGGC) (LUAla (GTGAG (L) (L) (L) (ACATC) (C) (ACATC)	430 77 53 135 119	,		TCTGTGATCGAATCATTGGGGAT :::       AlaValIleAlaGluSerIleArgMe	AGATG   ::: ysile:	TTCTTGAACCTGCTCTTGAAATCGTG :::::         ::: erValLysThrTyrGlnGluValAla	CCCCTO
aLeuGly aleuGly :::   :::   aSerGly aSerGly aSerGly aSerGly aSerGly aSerGly aSerGly				ATCATI	CCATAC	CTTGA!     GlnGl	CCTGTCTATG           ProValTyr-
-GGGCTCAGG      CGGCAAATCC :     ::: rGlyLySThr CGGTCAGCGCT SAlaPheVal CACCAACCAGC        PThrAsnAsnAsn				GGGGA : : LeArgM	AATGA ::::: :SerAs	ATCGT  ;;;  ValA1	GGCTT
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                                                                                            RESULT 11
US-08-557-122A-26
        Sequence 26, Application US/08557122A
Patent No. 5879664
GENERAL INFORMATION:
APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
                                                                                                                                                                           1007
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                    ---ThrGluAsnLysSerValAlaAsnAspLeuGluThrLysLeuArgArgLeuMetGly
                                                                                                                                                                                                                                                                                                                                    AlaTyrTyrArgPheAsnAspMetSerPheLysGlyLysAsnAsnLeuLysSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                  ArgSerSerGluLeuPheGluLeuGlyLeuLysHisLysLeuIleGlnLysThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------GATAAGAGGGTGGATGACATGCTTGCTGGGGCTCTTGGAG-----
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                                                                                                                                           ValValThrPro 416
                                                                                                                                                                        GTTCTTGAACCT 1018
                                                                                                                                                                                                        ThrGluAlaProLysGluGluAlaGluAspSerSerProSerAspLeuProGluGlu
                                                                                                                                                                                                                                      CCCATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCT 1006
                                                                                                                                                                                                                                                                                                    HisAlaProProPheLysThrAlaGlnPheGluLeuGluPheGly---LysGlyIleCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLysGluGlyGluGluThrIleGlySerGlnValAlaValLysIleValLysAsnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SerLeuSerLeuSerGlnThrValLeuLeuPheIleAsnGlnIleArgAlaLysValAla
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 3980
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                             1142
1162 nAsnPheGluGlyGluIleThrLysGluLysLeuLeuAspPheIleLysHisAsnGlnLe 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                             1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1028 AspAspIleProPheGlyLeuThrAlaSerSerAspAspAlaAlaAlaAlaGluThrLeu 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               1085 rSerSerAlaAspAspLeuProAlaTyrLeuAlaAsnGluThrPheValThrProValIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 10174-6401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                    CAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGAT
                                                                         rLysTyrGlnLeuAspLysAspGlyValValLeuPheLysLysPheAspGluGlyArgAs 1162
                                                                                                                                                      sHisPheAsnAspTyrAspPheValSerAlaGluAsnAla-----AspValPheSe
                                                                                                                                                                                           CAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTGC 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAspSerSerGlu-ValValValIleGlyPhePheLysAspValThrSerAspAlaAl
                                                                                                                                                                                                                                  eValGlnSerGlyLysIleAspAlaAspPheAsnAlaThrPheTyrSerMetAlaAsnLy
                                                                                                                                                                                                                                                                        TGCCCAAGAGCAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGAC 282
                                                                                                                                                                                                                                                                                                                                                                                         aLysGluPhe-----LeuLeuAlaAlaGluSerValAspAspIleProPheGlyIleSe 1085
                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTC--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACGGACCCTACCTCTTGTAGTGATTCTCGGGGGCACGGGCACCGGCAAATCCACGCTGGC 129
                                                                                                                                                                                                                                                                                                                                                    ----AGCGCTGACTCCATGCAGGTCTATGAAGGCCTAGACATCATCACCAACAAGGTTTC 222
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Matches:
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Indels:
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Sequence 26, Application US/09262666 Patent No. 6346244
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APPLICANT: Hjort, Carsten Mailand
TITLE OF INVENTION: Fungal Protein Disulfide Isomerase
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Best Local Similarity:
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 3052 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Lambiris, Elias
                         uPheLysLysPheAspGluGlyArgAsnAsnPheGluGlyGluValThrLysGluLysLe 1220
                                                                       TCACAAACGCCTA-
                                                                                                           uProLeu----ValIleValPheSerLysTyrGlnLeuAspLys----AspGlyValValLe
                                                                                                                                                         GGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACT
                                                                                                                                                                                                   nAsnPheGluGlyGluIleThrLysGluLysLeuLeuAspPheIleLysHisAsnGlnLe
                                                                                                                                                                                                                                                   CAATTATTACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGAT
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linear
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RESULT 12 US-09-262-666-26

COUNTRY: United States ZIP: 10174-6401 STATE: New York STREET: ADDRESSEE:

New York

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APPLICANT: DOCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1297
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DOCHERTY, ANDREW, J.P.
APPLICANT: SLOCOMBE, PARTICK, M.
TITLE OF INVENTION: A HUMAN METALLOPROTEINASE
TITLE OF INVENTION: VARIANTS THEREOF AND DNA S
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02109
                                                                                                                                                                                                                                                      STREET: 130 W
CITY: Boston
STATE: MA
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                                                    CLASSIFICATION:
                                                                   APPLICATION NUMBER: US/0 FILING DATE: 01-MAY-1997
                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                          USA
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13-MAR-1997
               PCT/GB96/02181
                                                                                     US/08/836,442
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DB:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-836-442-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
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FILING DATE: 21-DEC
APPLICATION NUMBER:
FILING DATE: 20-OCT
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                161
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APPLICATION NUMBER: GB 9518023.8
FILING DATE: 05-SEP-1995
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                                                                                                                          TTTCACAGACGCTATAATCAG-----
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             AsnGluAsnGlnAspGluIleArgLysArgValPheGluMetAlaAsnTyrValAsnMet
                                                TCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA----
                                                                                     GluHisGluLysTyrIleGluTyrTyrLeuValLeuAspAsnGlyGluPheLysArgTyr
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Alignment Scores:
                                         US-09-040-725A-1
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                                                                                                                   TITLE OF INVENTION: Parmaceutical composition containing TITLE OF INVENTION: on tyrosine 353 FILE REFERENCE: 39108200100 CURRENT APPLICATION NUMBER: US/09/040,725A CURRENT FILING DATE: 1998-03-18 NUMBER OF SEQ ID NOS: 4 SOFTWARE: Patentin Ver. 2.1 SECTIM. 506
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09040725A Patent No. 6399584 GENERAL INFORMATION:
                                                          LENGTH: 586
TYPE: PRT
ORGANISM: Homo:
                                                                                                                                                                                                                                                                                          APPLICANT:
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Gautreau, Alexis
Louvard, Daniel
                                                                                                                                                                                                                                                                                                                                                       Arpin, Monique
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                   ValMetThrAlaProProProProProProProValTyr--
                                                                                                                                             CACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAGACTAGTAACCAG-----CTT
                                                                                                                                                                                    GluAspGluValGluGluTrpGlnHisArgAla------LysGluAla 452
                                                                                                                                                                                                                                                                                                                                                                                            GluAlaAspArgMetAlaAlaLeuArgAlaLysGluGluLeuGluArgGln--
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                                                        CTAAAGAAAGGACCTGGTCCCATTGTCCCCCCTGTCTATGGCTTAGAGGTATCTGATGTC
                                                                                                                                                                                                                           ---GCTGGGCTCTTGGAGGAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTT
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                                                                                                                                                                                                                                                                    LysIleAlaLeuLeuGluGluAlaArg------
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US-09-513-151-3 (1-2041) x US-08-836-943-2 (1-739)	Watch: 2.63% Indels: Gaps:	Pred. No.: 0.266 Length: 739 Score: 94.00 Matches: 70 Percent Similarity: 37.248 Conservative: 57 Best Local Similarity: 20.53% Mismatches: 136	S.	WOLECULE TYPE: protein US-08-836-943-2	; LENGTH: 739 amino acids ; TYPE: amino acid ; TODDITORY. 11nar	INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:		REGISTRATION NUMBER: 26,963 REFERENCE/DOCKET NUMBER: 20357 TELECOMMUNICATION INFORMATION:	ATTORNEY AGENT INFORMATION:	APPLICATION NUMBER: US/08/836,943 FILING DATE: 08-MAY-1997	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:	C compatible	COMPUTER READABLE FORM:	H	<u>v</u>	R OF SEQUENCES: 3 SPONDENCE ADDRESS:	¥ ₹	; GENERAL INFORMATION: ; APPLICANT: Reinscheid, Dieter ; APPLICANT: Eikmanns, Bernhard ; APPLICANT: Sahm, Hermann	; Sequence 2, Application US/08836943 ; Patent No. 5965391	RESULT 15 US-08-836-943-2		1223 TCAGATGCTGTCAACACCATAGAAAGTCAGAGAGTGTTTCCCCAGACTATAACAAA 1276	QY 1103 GUAGUGUAGATAAAATUCGAATTGAACCAACTGAAGAAAAGAA	499TyrSerAlaGluLeuSerSerGluGlyIleArgAspAspArg	1103 AAGAGAAGTTA			QY 989 TCGAAGTGGGAGGAGTCTGTTCTTGAACCTGCTCTTGAAATCGTGCAAAGTTTCATCCAG 1048
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000 Let 000	9 CTA	869 GAATTTCACGAGTACCTGATCACTGAGGGAAAATGCACACTGGAGACTAGTAACCAGCTT 928 :::    :::     :::	619 IleLeuGlyTyrValValArgTrpValGiuHisGlyValGlyCysSerLysValPro 637	833TATCAACATGGTATCTTCCAATTGGCTTCAAG 868	9 ProAsnThrAsnTrpSerGluGluGluLysLysGluGluMetAspAsnAsnCysGlnSer	579 GluLeuArgAlaAlaGlyArgArgAspSerLeuArgAsnIleLeuThrIleProThrAla 598	GACATGCTTGCTGGGCCTCTTGGAGGAACTAAGA	686 ATCCTTTGGCTTCATGCTGACCAGGCAGTTCTAGATGAGCGCTTGGATAAGAGGGTTGAT /45 	3IleGlyGlnProArgGluGlyAlaAsnThrAlaTrpValProSerProThr	4 GGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGC::::	528 MetTrpAlaMetThrGluLeuMetAlaGluMetLeuGluLysLys 542	605CATAGTGAATTTCTCCATCGTCAACATACGGAAGAAGGT 643	:::	545 CCACATGACAAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCT 604	485 GGTCTTGTACTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCAT 544     :::::	2GlyPheLeuAspArgThrGlyAspGluIleHisThrSerMetGluAla	434 ATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGAT 484	389 GAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAG 433 ::::: :: :::::::::::::::::::::::::	6 ProArgHisThrLeuLysValGlyValMetAspGl	347 GACAAAATTCCTATTGTTGTGGGAGGAACCAATTATTACATT 388	ο.	287 TANAN ADAMPERANGE AND SELECTION OF THE SELECTION OF T	227 CAAGAGCAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAAT 286 336 Acricometaraacscarticg1:Garillalli	6 GluGlyIleMetAspAlaValLeuThrThrValCysAlaIleProGlyIleAlaProGln	_	:::	4 CAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCAGGTCTAT	89 GTGATTCTCGGGGCCACGGGCACC

Search completed: April 21, 2003, 18:52:17 Job time :  $42.0286\ \text{secs}$ 

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-MODEL-frame+_n2p.model -DEV=x1h
-MODEL-frame+_n2p.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26366/app_query.fasta_1.2446
-Q=/cgn2_1/USPTO_spool/US09513151/runat_15042003_141143_26366/app_query.fasta_1.2446
-QB-Swissprot_40 -QFMT=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09513151_@CGN.121_25_@runat_150402003_141143_26366 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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	Q9a6j5	P57632	Q98k j4	P38436	Q9jzr0	P74040	Q92hw4	Q9rtr6	025961	Q92nr2	Q9zjj7	P37724	051761	Q8z186	069967	Q8xdn3	P16384	Q9ph56	067162	Q8ziw3	Q9a059	Q9z6z6	Q97rw5	Q9juu5	033232	P46811	Q9p1f7
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## ALIGNMENTS

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P07884; Q12203;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
tRNA isopentenyltransferase (EC 2.5.1.8) (Isopentenyl-diphosphate:
tRNA isopentenyltransferase) (IPP transferase) (IPTase) (IPPT).
MOD5 OR YOR274W.
ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AND ALTERNATIVE AN
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE INITIATION, AND SUBCELLULAR LOCATION.
MEDLINE=92052176; PubMed=1946403;
Slusher L.B., Gillman E.C., Martin N.C., Hopper A.K.;
"mRNA leader length and initiation codon context deter
alternative AUG selection for the yeast gene MOD5.";
proc. Natl. Acad. Sci. U.S.A. 88:9789-9793(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheret G., Bernardi A., Sor F.J.;
"DNA sequence analysis of the VPH1-SNF2 region Saccharomyces cerevisiae.";
Yeast 12:1059-1064(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87172703; PubMed-3031457;
Najarian D., Dihanich M.E., Martin N.C., Hopper A.K.;
"DNA sequence and transcript mapping of MOD5: feature
region which suggest two translational starts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c;
MEDLINE=97051594; PubMed=8896271;
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EMBL; X89633; CAA61780.1; --
EMBL; Z75182; CAA99499.1; --
PIR; A26717; A26717.
SGD; S0005800; MOD5.
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                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRPAMS; TIGR00174; mlaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE INITIATION, AND SUBCELLULAR LOCATION.
MEDLINE-94187700; PubMed-8139535;
Boguta M., Hunter L.A., Shen W.C., Gillman E.C., Martin N.C.,
Hopper A.K.;
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; tRNA processing; ATP-binding; Alternative initiation; Mitochondrion; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: MITOCHONDRIAL, CYTOPLASMIC AND NUCLEAR.
ALTERNATIVE PRODUCTS: TWO ISOFORMS MAY BE PRODUCED FROM THE USE OF
ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                    GlyLysSerGlnLeuSerIleGlnLeuAlaGlnLysPheAsnGlyGluValIleAsnSer 45
                                                                             GGCAAATCCACGCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCT 172
                                                                                                       LeuLysGlyCysLeuAsnMetSerLysLysValIleValIleAlaGlyThrThrGlyVal
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MISSING (IN REF. 1).
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; A956B17ABC05161F CRC64;
                                                                                                                                                                                                                                                                                                                                         FOR CYTOPLASMIC/NUCLEAR ISOFORM ATP (POTENTIAL).
BINDS ISOPENTENYLPYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRIAL ISOFORM.
TRNA ISOPENTENYLTRANSFERASE, CYTOPLASMIC/
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1198 406	ATCATCATTGGGGATCGCGAATGGGCAGCGCACATAAAATCCCAAATCCCACTTGAACCAA :::      :::	1139 387	Qy Db
386	EuAspAspTrpThrHisTyrThrCysAsnValCysArgAsnAlaAspGlyLysAsnVal	367	ФФ
1138	⊅	1109	Qy
366	l  :::	. 347	Db
1108	aagctgagaacaagaga	1049	Qy
346	gProlleLysGln	327	Db
1048	CAG	1007	· Oy
326	spIleTyrLeuLeuAspAlaThrAspLeuSerGlnTrpAspThrAsn	307	Db
1006	TTAGAGGTATCTGATGTCTCGAAGTGGGAGGAGTCT	959	Qy
306	ThrargThrargGlnTyralaLysArgGlnValLysTrpIleLysLysMetLeuIlePro	287	Db
958	ACTAGTAACCAGCTTCTAAAGAAAGGACCTGGTCCCATTGTCCCC	905	Qy
286	ThrGlyLysThrAspAspAsnThrValLysLeuGluAspCysIleGluArgMetLys	268	Db
904		890	Qy
267	G	249	ф
889	GACTATCAACATGGTATCTTCCAATCAATTGGCTTCAAGGAATTTCACGAGTACCTGATC	830	Qy
248	GlnGluIleLysGlnLeuTyrGluTyrTyrSerGlnAsnLysPheThrProGlu	231	Дb
829	AGGAACTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCC	770	Qy
230	GluProLeuPheGlnArgLeuAspAspArgValAspAspMetLeuGluArgGlyAlaLeu	211	DЪ
769	GCAGTTCTAGATGAGCGCTTGGATAAGAGGTGGATGACATGCTTGCT	710	Qy
210	ThrLeuLysPheAspThrLeuPheLeuTrpLeuTyrSerLysPro	196	Db
709	CCCCTTGGAGGTCCTCTGAAGTTCTCTAACCCTTGCATCCTTTGGCTTCATGCTGACCAG	650	Qy
195	LysThrGlyLysLysProSerGluThrPheAsnGluGlnLysIle	181	ДD
649	CATAGTGAATTTCTCCATC	590	Qy
180	AlaThrLysTyrHisProAsnAspTyrArgArgValGlnArgMetLeuGluIleTyrTyr	161	מם
589	GCTGCCAAGCTGCATCCACATGACAAACGCAAAGTGGCCAAGGAGCTTGCAAGTTTTTGAA	530	Qy
160	LeuGluSerThrAspProAspValIleTyrAsnThrLeuValLysCysAspProAspIle	141	Дb
529	GAAAT	470	Qy
140	ValAspThrLysSerSerGluArgLysLeuThrArgLysGlnLeuAspIle	124	Db
469	GTCAATACCAAGCCCCCAGGAGATGGGCACTGAGAAAGTGATTGACCGAAAAGTGGAG	413	Оу
123	lleProIleValValGlyGlyThrHisTyrTyrLeuGlnThrLeuPheAsnLysArg	105	Db
412		353	Qy
104		85	ДD
352	GTGGTGGACTTCAGAAATAGAGCAACTGCTCTGATTGAAGATATATTTTGCCCCGAGACAAA	293	Оу
84	argGluGlyIleProHisHisValMetAsnHisValAspTrpSerGluGluTyrTyr	66	da
292	CAGAGAATCTGCCGGCACCACATGATCAGCTTTGTGGATCCTCTTGTGACCAATTACACA	233	Qy

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16-OCT-2001
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InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT. 1.
ProDom; PD004674; IPPT; 1.
TIGRFAMS; TIGR00174; miah; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  halodurans and genomic sequence comparison with Bacillus subtilis.";

Nucleic Acids Res. 28:4317-4331(2000).

-i- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF

2-METHYLTHIO-N6-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]1[6]A])

ADJACENT TO THE ANTICODON OF SEVERAL TRAN SPECIES (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate +

tRNA containing 6-isopentenyladenosine.

-i- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus halodurans.
Bacteria; Firmicutes;
NCBI_TaxID=86665;
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MEDLINE=20512582; PubMed=11058132;
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(IPTase) (IPPT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takami H., Nakasone K., Takaki Y., Maeno G.,
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                                               LysArgLeuAsnGlyGluValIleSerGlyAspSerMetGlnValTyrArgGlyMetAsp
                                                                                                          LeuValAlaIleValGlyProThrAlaValGlyLysThrLysThrSerValMetLeuAla
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                                                                                                                                                                                                                                                                                                                                  314 AA;
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
2)-isopentenylpyrophosphate transferase (EC 2.5.1.
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417.00
56.27%
34.58%
11.66%
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Matches:
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bollotin A., Borchert Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., B Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel
                                                                                                                                                                                                                                                                                                                   MIAA_BACSU 031795;
                                                                                  MEDLINE=98044033; PubMed=9384377;
                                                                                                     STRAIN-168
                                                                                                                                               Bacteria; Firmicutes;
NCBI_TaxID=1423;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                   Bacillus subtilis
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RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
AJOris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Hobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinols S., Lauber J., Lazarevic V.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medique C.,
RA Kodina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tanconi E., Takagi T., Takahashi H., Takemaru K.,
RA Yoshida K., Voshikawa S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus RT. Nature 2007-246-256-1007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SubtiList; BG12617; miaA.
InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRPAMS; TIGR00174; miaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 390:249-256(1997).

-I- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF 2-METHYLITHIO-N6-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])

ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: Isopentenyl diphosphate + trna - diphosphate + tRNA containing 6-isopentenyladenosine.

-I- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Denizot F., Devine K.M., Dusterhoft A., Ehrlich S
Entian K.D., Errington J., Fabret C., Ferrari E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase; Nucleotidyltransferase; tRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 299113; CAB13617.1; -.
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AspIleGlyThrAlaLysIleThrGluGlnGluMetGluGlyValProHisHisLeuIle
                                                                                                                                                                        GACATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAATCTGCCGGCACCACATGATC
                                                                                    alaLysSerLeuAsnAlaGluIleIleSerGlyAspSerMetGlnIleTyrLysGlyMet
                                                                                                                                GGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCCTGACTCCATGCAGGTCTATGAAGGCCTA
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403.50
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Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A., Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T., Charbit A., Chetouani F., Couve E., Daruvar A., Dehoux P., Domann E., Domlnguez-Bernal G., Duchaud E., Durant L., Dussur; Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P., Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jack:
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I
                                                                                                                                                                              STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
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Bacteria; Firmicutes;
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Science 294:849-852(2001).

1- FUNTION: Catalyzes the first step in the biosynthesis of 2-methylthio-NG-(delta(2)-isopentenyl)-adenosine (MS[2]I[6]A]) adjacent to the anticodon of several tRNA species (By similarity).

1- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate - tRNA - diphosphate
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ProDom; PD004674; IPPT; 1.
TIGRFAMS; TIGR00174; miaA; 1.
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Pfam; PF01715; IPPT;
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Madueno E., Maitournam A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ListiList; LMO01294;
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SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
CACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATGACAAA
                                                                                                                                                        GlyLeuTyrIleGlnSerValPheTyrAspTyrAspPheGlyAsnValSerGluAspLys 122
                                                                                                                                                                                                                                                           ArgLysTrpIleGluThrIleH1sGlnAlaGlyLysLeuProIleIleValGlyGlyThr
                                                                                                                                                                                                                                                                                                                                                                          IleAspValThrAspPro---SerGluProPheThrAlaAlaLysPheGlnThrGluThr
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                                                                                                                                                                                                                                                                                                                  305 AA;
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34833 MW;
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edjari H.,
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Q92C59;
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   use by modified
                                                            between
the Euro
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
(IPPase) (IPPT)
                                                                                                                                                                                                                                                                                                                                                                "Comparative genomics of Listeria species."; Science 294:849-852(2001).
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MEDLINE-21537279; PubMed-11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Bacteria; Firmicutes;
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                                                                                                                                                                                                                                           FUNCTION: Catalyzes the first step in the biosynthesis of 2-methylthio-N6-(delta(2)-isopentenyl)-adenostine (MS[2]I[6]A]) adjacent to the anticodon of several tRNA species (By similarity). CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate +
                                                                                                                                                                                  tRNA containing 6-isopentenyladenosine. SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                         European
                               SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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ProDom; PD004674; IPPT; 1.
TIGRRAMS; TIGR00174; miaA; 1.
Transferase; Nucleotidyltransferase; tRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@lsb-sib.ch).
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SEQUENCE 305 AA;
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TATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATC-----
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RESULT 6
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Best Local Similarity:
                                                                                                                             Score:
                                                                                                                                                          Alignment
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Moelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
-! FUNCTION: Catalyzes the first step in the biosynthesis of 2-
methylthio-NG-(delta(2)-isopentenyl)-adenosine (MS[2][6]A])
adjacent to the anticodon of several tRNA species (By similarity).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate +
                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                     Complete proteome. NP_BIND 9
                                                                                                                                                                                                                                                                Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tRNA containing 6-isopentenyladenosine.
-!- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
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Bacteria; Firmicutes; Clost
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
trNA delta(2)-isopentenylpyrophosphate transferase (EC
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15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IF
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
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Bacteria; Firmicutes; Clostridia;
Clostridium
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proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS[2]I[6]A])
methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS[2]I[6]A])
adjacent to the anticodon of several trNA species (By similarity).
-!- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
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SEQUENCE 310 AA;
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Pfam; PF01715; IPPT; 1.

ProDom; PP004674; IPPT; 1.

TIGRPAMS; TIGR00174; miaA; 1.

Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding;
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Shiba T., Ogasawara N., Hattori M., Kuhara S., I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tRNA containing 6-isopentenyladenosine. SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
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AspLysAspGluGluTyrArgGluGluLeuGluLysIleAlaAsnGluHisGlyAsnGlu 137
                                    GAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAG-----GAGGATGGT---CTT 490
                                                                                                  TACATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACT 442
                                                                                                                                                LysIleLysAspIleGlnSerArgGlyLysLeuProIleLeuValGlyGlyThrGlyLeu 103
                                                                                                                                                                                                                                                              TTTGTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCT
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1. FUNCTION: Catalyzes the first step in the biosynthesis of 2-methylthio-NG-(delta(2)-isopentenyl)-adenosine (MS[2]I[6]A]) adjacent to the anticodon of several tRNA species (By similarity).

1. CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = dipho
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
(IPTase) (IPPT).
MIAA OR RSC2564 OR RS00755.
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Bacteria; Proteobacteria; beta subdivision; Ralst
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SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
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                                                 gLeuHisAlaThrAspAlaGlnArgIleGlnArgAlaLeuGluLeuTyrArgLeuThrGl
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                                                                                                                   US-09-513-151-3 (1-2041) x MIAA_PSEPU (1-322)
                                                                                                                                                                     Query Match:
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                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 olekhnovich I.N., Gussin G.N.;

*Attenuation of the Pseudomonas putida trpE and trpGDC genes.";

submitted (JUL-1997) to the EMEL/GenBank/DDBJ databases.

-I-FUNCTION: CATALYZES THE FIRST STEE IN THE BIOSYNTHESIS OF

2-METHYLIHIO-NS-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])

ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).

-I-CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
trNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
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30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas putida.
Bacteria; Proteobacteria;
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ProDom; PD004674; IPPT; 1.
TIGRFAMS; TIGR00174; m1aA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
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SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
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SEQUENCE FROM N.A. STRAIN-MSB8 / DSM MEDLINE-99287316;
                                                                                                                                     transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
(IPTase) (IPPT)
MIAA OR TM0525.
                                                                                                                                                                                      16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC
                                                                                 Bacteria; Thermotogae; Thermotogaceae; Thermotogaceae; Thermotoga
                                                                 NCBI_TaxID=2336;
                                                                                                                   Thermotoga maritima
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   PubMed=10360571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Helson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Salzberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RI Mature 399:323-329(1999).
C-I- FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF 2-
METHYLTHIO-NG-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])
CC METHYLTHIO-NG-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])
CC ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])
CC -I- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity: Y Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRRAMS; TIGR00174; miaA; 1.
Transferase; Nucleotidyltransferase; tRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
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                                                                GlyLeuTyrAlaAspAlaLeuVal···ArgGlyIlePheGluGlyValProAlaAspGlu
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                                GGCACTGAGAAAGTGATTGACCGAAAAGTGGAGCTTGAAAAGGAGGATGGTCTTGTACTT
                                                                                                                                                       IleAspIleIleAspPro---AspGluTyrTyrAsnAlaPheMetTyrArgLysAspSer
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                                                                                                                                    LeuArgAlaMetGluAspValLeuArgArgGlyLysIleProValTyrValGlyGlyThr
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Matches:
Conservative:
Mismatches:
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RESULT 11

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                                                                          the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    Science 282:754-759(1998).

1: FUNCTION: CATALYZES THE FIRST STEP IN THE BIOSYNTHESIS OF

2-METHYLTHIO.NG-(DELTA(2)-ISOPENTENYL)-ADENOSINE (MS[2]I[6]A])

ADJACENT TO THE ANTICODON OF SEVERAL TRNA SPECIES (BY SIMILARITY).

1: CATALYTIC ACTIVITY: Isopentenyl diphosphate + trna = diphosphate +

trna containing 6-isopentenyladenosine.

1: SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                         EMBL; AE001349; AAC68361.1;
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-D/UW-3/CX;
STRAIN-99000809; pubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J.,
Stephens R.S., Kalman S., Tatusov R.L.
  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
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MIAA OR CT766.
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NP_BIND 11
SEQUENCE 314 AA;
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TIGRPAMS; TIGR00174; miah; 1.
Transferase; Nucleotidyltransferase; tRNA processing;
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AlaIleGlyTyrArgGluTrpIleGluPheLeuAspLeuGlySerProProAspLeuPhe
                              TCAATTGGCTTCAAGGAATTTCACGAGTACCTG
                                                               AlaGlyIleLysGlyAsnSerSerAlaSer---
                                                                                              CGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTATCAACATGGTATCTTCCAA 853
                                                                                                                              AAGAGGGTGGATGACATGCTTGCTGCGGCTCTTGGAGGAACTAAGAGATTTTCACAGA
                                                                                                                                                                                               TyrHisCysArgArgTrpLeuLeuSerProAspProGluLeuLeuArgHisAsnIleLeu
                                                                                                                                                                                                                            AACCCTTGCATCCTTTGG----CTTCATGCTGACCAGGCAGTTCTAGATGAGCGCTTGGAT 733
                                                                                                                                                                                                                                                             AlaTrpGlnSerThrValAsnGluSerLys----
                                                                                                                                                                                                                                                                                             CTCCATCGTCAACATACGGAAGAAGGTGGTGGTCCCCTTGGAGGTCCTCTGAAGTTCTCT 676
                                                                                                                                                                                                                                                                                                                            AsnLysIleIleArgAlaLeuGluIleIleArgLysThrGlySerLysValSerSerTyr 179
                                                                                                                                                                                                                                                                                                                                                         CGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAATTT 616
                                                                                                                                                                                                                                                                                                                                                                                           TyrGlnGluLeuGluLeuLeuAspProValTyrAlaAlaThrIleThrLysHisAspLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspPheValLeuArgGluGlnLeuThrLeuGluAlaGlnGluArgGlyIleSerAlaLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAAAGTGATTGACCGAAAAGTGGAGCTTGAA---AAGGAGGATGGTCTT---GTACTT 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaCysGlnAspIleLeuSerArgAsnLysValProIleLeuValGlyGlyThrGlyPhe 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGATTGAAGATATTTTGCCCGAGACAAAATTCCTATTGTTGTGGGAGGAACCAATTAT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ValCysHisValGlnGluSerPheAsnAlaValAspPheTyrTyrHisAlaValGln
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Conservative:
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                                                                                                                        US-09-513-151-3 (1-2041) x MIAA_PASMU
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Q9CMC7;
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15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of Pasteurella multocida Pm70.";

Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-- FUNCTION: Catalyzes the first step in the biosynthesis of 2-methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS[2]I[6]A])

adjacent to the anticodon of several tRNA species (By similarity).

--- CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA = diphosphate +

tRNA containing 6-isopentenyl diphosphate FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
trNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (IPP
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
                                                                                                                                                                                                                                                                                             Complete proteome. NP_BIND 13
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRFAMS; TIGR00174; miaA; 1.
                                                                                                                                                                                                                                                                                                                          Transferase; Nucleotidyltransferase; tRNA processing; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006129; AAK02989.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Pm70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=747;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pasteurella multocida
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                                                                                                                                                                                                                                                                                                                                                                                                                                      send an email to license@isb-sib.ch).
                                                                           CCTGCAACGGACCCTACCTCTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCAC
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                             GCTGGCGTTGCAGCTAGGCCAGCGGCTCGGCGGTGAGATCGTCAGCGCTGACTCCATGCA 183
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Matches:
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Indels:
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         Staphylococcus aureus (strain Mu50 / ATCC 700699) Staphylococcus aureus (strain N315), and Staphylococcus aureus (strain MW2). Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                    MIAA_STAAM STANDARD; PRT; 311 AA.
099UH0;
099UH0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2:5.1.8) (I)
transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
(IPTase) (IPPT).
MIAA OR SAVI304 OR SA1144 OR MW1186.
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                                                                                                                                                                                                                                                   Query Match:
                                                                                                                                                                                                                                                                                                   Score:
                                                                                                                                                                                                                                                                                                                      Alignment Pred. No.
                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MASO / ARCC 700699, and N315;
MEDLINE-21311952; PubMed-11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., S., Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.; "Mhole genome sequencing of meticillin-resistant Staphylococcu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP003361; BAB57466.1; -.
EMBL; AP003133; BAB42398.1; -.
EMBL; AP004826; BAB95051.1; -.
Interpro; IPR002627; IPPT,
Pfam; PF01715; IPPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
STRAIN-MU50 / ATCC
                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. NP_BIND 13
                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD004674; IPPT; 1. TIGRFAMS; TIGRO0174; miaA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22040717; PubMed-12044378;
Baba T., Takeuchi F., Kuroda M., Yuzawa
Nagai Y., Iwama N., Asano K., Naimi T.,
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tRNA containing 6-isopentenyladenosine.
-!- SIMILARITY: BELONGS TO THE IPP TRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired MRSA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aureus
                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Nucleotidyltransferase; tRNA processing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lancet 359:1819-1827(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                    203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Catalyzes the first step in the biosynthesis of 2-methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS[2]1[6]A]) adjacent to the anticodon of several tRNA species (By similarity) CATALYTIC ACTIVITY: Isopentenyl diphosphate + tRNA - diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Catalyzes the first step in the biosynthe methylthio-N6-(delta(2)-isopentenyl)-adenosine (MS)
                                                                                    ATCATCACCAACAAGGTTTCTGCCCAAGAGCAGAATCTGCCGGCACCACATGATCAGC
                                                                                                                               CTTGTAGTGATTCTCGGGGCCACGGGCACCGGCAAATCCACGCTGGCGTTGCAGCTAGGC
                                                                                                                                                                                                                                                                                                                                    Scores:
IleGlyThrAlaLysValThrProGluGluMetAspGlyIleProHisHisLeuIleAsp
                                                               LysArgIleAsnGlyGluIleIleSerGlyAspSerMetGlnValTyrLysHisMetAsn
                                                                                                                                                                                                                                                                     Similarity:
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339.00
55.64%
32.33%
9.48%
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35868 MW;
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; 6011E9D44878043E
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                                                                                                                                                                                                                                                                                                  Length: Matches:
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Kuroda H., Cui
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Ito T.,
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                                   SEQUENCE FROM N.A.

STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630 PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,

Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
tRNA delta(2)-isopentenylpyrophosphate transferase (EC 2.5.1.8) (I transferase) (Isopentenyl-diphosphate:tRNA isopentenyltransferase)
                                                                                                                                                                                                                                                                                                                                    MIAA OR TRPX OR H10068.
Haemophilus influenzae.
Bacteria; Proteobacteria;
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Whole-genome random sequencing and
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AlaIleGlyTyrLysGlu
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  assembly of Haemophilus influenzae
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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pfam; PF01715; IrPT; 1.
ProDom; PD004674; IPPT; 1.
TIGRFAMS; TIGR00174; miaA; 1.
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 158
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                                                                                                                                                                                                                                                                                                                                                                                    26 GlnLeuProValGluValIleSerValAspSerAlaLeuIleTyrLysGlyMetAspIle
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                                                                                                                                                                               ATTGAATCTCTGCTCTGGAAAGTTCTTGTCAATACCAAGCCCCAGGAGATGGGCACTGAG 445
                                                                                                                                                                                                                   GTGGATCCTCTTGTGACCAATTACACAGTGGTGGACTTCAGAAATAGAGCAACTGCTCTG 325
                                                                                                                                                                                                                                                                                                                                 GlyThrAlaLysProSerLysGluGluLeuAlaLeuAlaProHisArgLeuIleAspIle
                                                                                                                                                                                                                                                                                                                                                           ATCACCAACAAGGTTTCTGCCCAAGAGCAGAGAATCTGCCGGCACCACATGATCAGCTTT
                         AAACGCAAAGTGGCCAGGAGCTTGCAAGTTTTTGAAGAAACAGGAATCTCTCATAGTGAA 613
                                                                                CTTCACAAACGCCTAAGCCAGGTGGACCCAGAAATGGCTGCCAAGCTGCATCCACATGAC
                                                                                                                                    AAAGTGATTGACCGAAAAGTGGAGCTTGAA----
                                                                                                                                                                TyrLysAlaLeu
                                                                                                                                                                                                                                                LeuAspPro---SerGluSerTyrSerAlaMetAsnPheArgAspAspAlaLeuArgGlu
                                                      LeuHisThrGluLeuAlaLysIleAspProIleSerAlaAlaArgIleAsnProSerAsp
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334.50
51.52%
31.31%
9.36%
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                                                                                                            ArgAlaGluLeuGluGlnLysAlaAlaGlnGlnGlyTrpAlaAla
                                                                                                                                                                  ---IleGluGlyLeuSerProLeuProSerAlaAspGlu
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Indels:
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Matches:
Conservative:
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                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-El Tor N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.

McDonald L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          09KV12;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
trnA delta(2)-isopentenylpyrophosphate transferase (EC
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(IPTase) (IPPT).
MIAA OR VC0346.
                                  EMBL; AE004123; AAF93519.1; TIGR; VC0346; -.
              InterPro; IPR002627; IPPT.
Pfam; PF01715; IPPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIAA_VIBCH
                                                                                                                                                                                                                                                DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-666;
                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                   /ibrio cholerae.
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                                                                                                                European Bioinformatics Institute.
                                                                                                         SWISS-PROT entry is copyright. It is produced through a collabeen the Swiss Institute of Bioinformatics and the EMBL outsteen the Swiss Institute. There are no restrictions
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 ATCACTGAGGGAAAATGCACACTGGAG
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Best Local Similarity:
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Transferase; Nucleotidyltransferase; tRNA processing;
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LeuHisProAspLeuProSerIleArgCysValGlyTyrArgGlnMetTrpAspTyrLeu
                                         CAACATGGTATCTTCCAATCAATT--
                                                                                                                         CTAAGAGATTTTCACAGACGCTATAATCAGAAGAATGTTTCGGAAAATAGCCAGGACTAT
                                                                                                                                                                                                         -----AlaProLysGluArgAlaGlu
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                                                                                                                                                                                                                                                                                                                                  GlyLysThrLeuThrGluLeu----
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                                                                                                                                                                  LeuHisArgArgIleGluLeuArgPheGluLysMetValGluSerGlyPheGluGluGlu
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